

Db 61 RFVVDLHHCIAKRWIAQRGVAALNLGNGPLNVLVGLGVLLGQFVYRFRFFKS 116

RESULT 14

AA0765127 standard; protein; 52 AA.

AC AAB35127;

DT 03-APR-2001 (first entry)

DE Mammalian Bak alpha-5 and alpha-6 helices.

KM Mammal; Bax; apoptosis modulator; BCL-2.

OS Mammalia.

PN US6165732-A.

PD 26-DEC-2000.

PF 31-JUL-1998; 98US-0127048.

PR 14-OCT-1997; 97US-0061823.

PA (UNIM) UNIV WASHINGTON.

PI Korsmeyer SJ, Schlesinger PH;

DR WPI: 2001-101692/11.

PT Identifying apoptosis-modulating compounds by contacting the compound with lipid bilayer containing an ion channel formed by anti-apoptotic polypeptide of Bcl-2 family and determining ion selectivity of the channel -

PS Example 7; Fig 7; 34pp: English.

CC The present invention describes a method for identifying modulators of apoptosis which involves contacting a compound of interest with a lipid bilayer comprising a K⁺ or Cl⁻ selective channel. This channel is a member of the BCL-2 family. Apoptosis modulators are also provided, including Bcl-2deltaTAM and BaxdeltaTAM.

CC Sequence 52 AA;

Query Match 25.7%; Score 284; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDLHHCIAKRWIAQR 174

Db 1 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDLHHCIAKRWIAQR 52

RESULT 15

AA076550 standard; Protein; 52 AA.

AC AA076550;

DT 08-MAY-2002 (first entry)

DE Murine Bak peptide containing helices alpha-5 and alpha-6.

KM Mouse; Bak; alpha-5 helix; alpha-6 helix; BCL-2; apoptosis modulation; neoplasia; Epstein-Barr virus; African swine fever virus; adenovirus;

KM lymphoproliferative condition; cancer; arthritis; Crohn's disease; wound; inflammation; autoimmune disease; immunodeficiency disease; senescence;

KM neurodegenerative disease; ischaemic cell death; reperfusion cell death; infertility; apoptosis-promoting peptide.

OS Mus sp.

XX PN WO200205835-A2.

XX PD 24-JAN-2002.

XX PF 25-JUN-2001; 2001WO-US20169.

XX PR 17-JUL-2000; 2000US-0617878.

XX PA (UNIM) UNIV WASHINGTON.

XX PI Korsmeyer SJ, Schlesinger PH;

XX DR WPI: 2002-179747/23.

PT Identifying apoptosis modulating compounds for treating e.g. cancer, comprises contacting a lipid membrane with a pore-forming BCL-2 member and test compound, and determining if formation of large pores in the membrane is regulated -

PS Example 7; Fig 7; 70pp: English.

CC The invention relates to a method for identifying apoptosis modulating compounds, involving contacting a lipid membrane with a pore-forming pro-apoptotic BCL-2 family member and a test compound, and determining whether the compound regulates formation of large pores in the lipid membrane. An increase in the number of large pores in the lipid membrane indicates that the compound is an apoptosis promoter and a decrease in the number of large pores indicates that it is an apoptosis inhibitor. Apoptosis modulating compounds are useful for inducing or inhibiting apoptosis in a cell, to treat a patient having a condition mediated by excessive down-regulation of apoptosis (such as neoplasias, diseases caused by Epstein-Barr virus, African swine fever virus and adenovirus, CC lymphoproliferative conditions, cancer, arthritis, Crohn's disease, CC inflammation and autoimmune diseases), or excessive apoptosis (such as immunodeficiency diseases, senescence, neurodegenerative diseases, CC ischaemic and reperfusion cell death, infertility and wounds. This CC sequence represents a mouse Bak apoptosis-promoting peptide containing the alpha-5 and alpha-6 helices, used in the methods of the invention.

CC Sequence 52 AA;

Query Match 25.7%; Score 284; DB 23; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDLHHCIAKRWIAQR 174

Db 1 INMGVVALLGFGYRLALHYOHGLTGFLGQVTRFVVDLHHCIAKRWIAQR 52

Search completed: March 27, 2003, 10:52:30
Job time : 75 secs

SQ Sequence 117 AA;

Query Match 56.7%; Score 625; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1e-60;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 MGQVGRQALITGDDINRRYDSFQTMLOHPTAENAYEFTKIATSLFESGIMNGRYVA 130
 |||||||
 DB 1 MGQVGRQALITGDDINRRYDSFQTMLOHPTAENAYEFTKIATSLFESGIMNGRYVA 60

OY 131 LIGFSGYRALAHYQHGLTGFGLGQVTRFYVDLHHCIARWIAQRGWAALNLGNP 187
 |||||||
 DB 61 LIGFSGYRALAHYQHGLTGFGLGQVTRFYVDLHHCIARWIAQRGWAALNLGNP 117

RESULT 12

AAW77881

ID AAR77881 standard; Protein; 116 AA.

AAW77881;

DT 21-NOV-1995 (first entry)

DE Human Cdn-1(96-211).

XX Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.

OS Homo sapiens.

PN WO9515084-A.

PD 08-JUN-1995.

PF 30-NOV-1994; 94WO-US13930.

PR 07-OCT-1994; 94US-0320157.

PR 30-NOV-1993; 93US-0160067.

PA (LXRB-) LXR BIOTECHNOLOGY INC.

PI Barr PJ, Kiefer MC;

PI Barr PJ, Kiefer MC;

XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.

PS Disclosure; Fig. 11; 66pp; English.

XX Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Truncated Cdn-1 derivatives given in AAR77879-81 were used to
 CC test the effects of deleting the N-terminal sequences of Cdn-1
 CC on this activity.

SQ Sequence 116 AA;

Query Match 55.2%; Score 609; DB 16; Length 116;
 Best Local Similarity 100.0%; Pred. No. 5.8e-59;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 MLOHLOPTAENAYEFTKIATSLFESGIMNGRYVALLGFGYRALAHYQHGLTGFGLGQVT 155
 |||||||

DB 1 MLOHLOPTAENAYEFTKIATSLFESGIMNGRYVALLGFGYRALAHYQHGLTGFGLGQVT 60

OY 156 RFVVDLHHCIARWIAQRGWAALNLGNPILNLVVLGVLLGQFYVRRFFKS 211
 |||||||

DB 61 RFVVDLHHCIARWIAQRGWAALNLGNPILNLVVLGVLLGQFYVRRFFKS 116

RESULT 13

AAW79536

ID AAW79536 standard; Protein; 116 AA.

AAW79536;

DT 11-JAN-1999 (first entry)

DE Truncated Bak polypeptide Bak-delta3.

XX Bak; bak binding protein; BBP; bbpbd-1; bbpbd-2; Bel-2; apoptosis;
 KW cell death; cancer; lymphoma; neurodegeneration; heart disease;
 KW cell proliferation; infection; human; therapy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 8..31 /label= BBPBD-1

FT Peptide 43..61 /note= "Claim 36"

FT Peptide /label= BBPBD-2

FT /note= "Claim 62"

PN WO9841626-A1.

PD 24-SEP-1998.

PF 03-MAR-1998; 98WO-US04079.

PR 09-JAN-1998; 98US-0071097.

PR 20-MAR-1997; 97US-0041328.

PA (LXRB-) LXR BIOTECHNOLOGY INC.

PI Barr PJ, Fitzpatrick PA, Gibson HL, Kiefer MC;

PI Barr PJ, Fitzpatrick PA, Gibson HL, Kiefer MC;

XX New Bak-binding protein and related nucleic acid, vectors,
 PT transformed cells and antibodies - are useful for modulation of
 PT apoptosis in cancer, neuro-degeneration etc., also peptide fragments
 PT of Bak that interact with the protein

PS Example 5; Page 54; 77pp; English.

XX This is the amino acid sequence of Bak-delta3, an N-terminal
 CC deletion mutant of Bak (see AAW79534) comprising amino acids 96-210
 CC of the full-length protein. PCR amplified Bak-delta3 was subcloned
 CC into vector pBluebacII and used in experiments to determine
 CC the interaction between Bak and a novel Bak binding protein (BBP,
 CC see AAW79537). The results indicated that Bak-delta3 is capable
 CC of interaction with loop 1 of BBP but not with the hydrophilic
 CC region represented by BBP loop 2. Bak-delta3 includes the claimed
 CC BBP binding domains of BBP but not with the hydrophilic
 CC domains of Bak. The invention relates to BBP, the gene encoding
 CC BBP (see AAW61499), methods for detecting substances that alter the
 CC specific binding between Bak and BBP, as well as diagnostic and
 CC therapeutic methods utilizing BBP.

SQ Sequence 116 AA;

Query Match 55.2%; Score 609; DB 19; Length 116;
 Best Local Similarity 100.0%; Pred. No. 5.8e-59;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 MLOHLOPTAENAYEFTKIATSLFESGIMNGRYVALLGFGYRALAHYQHGLTGFGLGQVT 155
 |||||||

DB 1 MLOHLOPTAENAYEFTKIATSLFESGIMNGRYVALLGFGYRALAHYQHGLTGFGLGQVT 60

OY 156 RFVVDLHHCIARWIAQRGWAALNLGNPILNLVVLGVLLGQFYVRRFFKS 211
 |||||||

XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX
 PS Disclosure; Fig.11; 66pp; English.
 XX
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly
 CC decreased this activity, suggesting that small, truncated Cdn-1
 CC molecules may be potent therapeutics.
 CC
 SQ Sequence 152 AA;

Query Match 71.7%; Score 791; DB 16; Length 152;
 Best Local Similarity 100.0%; Pred. No. 7,8e-79;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 MVTLPLOPSSSTMGQVGRQALITGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLF 119
 DB 1 MVTLPLOPSSSTMGQVGRQALITGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLF 60
 QY 120 ESGINMGVVALLGFGYRLAHYOHGTLGFGVTRFVVDMLHRCIARWIAORCGWVA 179
 DB 61 ESGINMGVVALLGFGYRLAHYOHGTLGFGVTRFVVDMLHRCIARWIAORCGWVA 120
 QY 180 ALNIGNPIINVLVLGVLLGQFVVRPFKS 211
 DB 121 ALNIGNPIINVLVLGVLLGQFVVRPFKS 152

RESULT 10

AAR77880
 ID AAR77880 standard; Protein; 141 AA.

XX AAR77880;
 AC
 XX
 DT 21-NOV-1995 (first entry)
 XX
 DE Human Cdn-1(71-211).
 XX
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 XX
 OS Homo sapiens.
 XX
 PN WO9515084-A.
 XX
 PD 08-JUN-1995.
 XX
 PF 30-NOV-1994; 94WO-US13930.
 XX
 PR 07-OCT-1994; 94US-0320157.
 PR 30-NOV-1993; 93US-0160067.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI; 1995-215106/28.
 XX

PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX

PS Disclosure; Fig.11; 66pp; English.

CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC

CC Deletion of the N-terminal 70 amino acids of Cdn-1 improved this
 CC activity, suggesting that small, truncated Cdn-1 molecules may be
 CC potent therapeutics.
 CC
 SQ Sequence 141 AA;

Query Match 66.8%; Score 737; DB 16; Length 141;
 Best Local Similarity 100.0%; Pred. No. 6,2e-73;
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 MGQVGRQALITGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFESGINMGWVA 130
 DB 1 MGQVGRQALITGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFESGINMGWVA 60
 QY 131 LIGFGYRLAHYOHGTLGFGVTRFVVDMLHRCIARWIAORCGWVAALNLNGPILN 190
 DB 61 LIGFGYRLAHYOHGTLGFGVTRFVVDMLHRCIARWIAORCGWVAALNLNGPILN 120
 QY 191 VLVLGVLLGQFVVRPFKS 211
 DB 121 VLVLGVLLGQFVVRPFKS 141

RESULT 11

AAW79535
 ID AAW79535 standard; Protein; 117 AA.

XX AAW79535;
 AC
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Truncated Bak polypeptide Bak-delta2-TM.
 XX
 KW Bak; bak binding protein; BBP; bbbpd-1; bbbpd-2; Bcl-2; apoptosis;
 KW cell death; cancer; lymphoma; neurodegeneration; heart disease;
 KW cell proliferation; infection; human; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9841626-A1.
 XX
 PD 24-SEP-1998.
 XX
 PF 03-MAR-1998; 98WO-US04079.
 XX
 PR 09-JAN-1998; 98US-0071097.
 PR 20-MAR-1997; 97US-0041328.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Fitzpatrick PA, Gibson HL, Kiefer MC;
 XX
 DR WPI; 1998-521220/44.
 XX

PT New Bak-binding protein and related nucleic acid, vectors,
 PT transformed cells and antibodies - are useful for modulation of
 PT apoptosis in cancer, neuro-degeneration etc., also peptide fragments
 PT of Bak that interact with the protein
 XX

PS Example 1; Page 53; 77pp; English.

CC This is the amino acid sequence of Bak-delta2-TM, a truncated
 CC polypeptide comprising amino acids 71-187 of Bak (see AAW79534).
 CC A nucleotide sequence encoding Bak-delta2-TM was obtained from
 CC cDNA by PCR and cloned as an in-frame fusion to the GAL4-DNA
 CC binding domain in vector PAS2-1. The construct was used in a
 CC two-hybrid screen of human heart cDNA for the identification of
 CC clones encoding Bak binding proteins. The invention relates to a
 CC novel Bak binding protein (BBP, see AAW79537), the gene encoding BBP
 CC (see AAW61499), methods for detecting substances that alter the
 CC specific binding between Bak and BBP, as well as diagnostic and
 CC therapeutic methods utilizing BBP.
 CC

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XX DR WPI; 1996-485886/48.
XX DR N-PSDB; AAT42139.
XX PT Screening for anti-viral agents - by detecting the ability of an
XX PT agent to disrupt the interaction of a Bak protein and a viral
XX PT protein
XX PS Disclosure; Fig 2; 24pp; English.
XX CC This Bak-2 protein sequence represents a bcl-1 homologue which
XX CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
XX CC protein, and is capable of modulating apoptosis. The protein may
XX CC be used in complete or partial form, or as an epitope tag fusion
XX CC protein, in a new virucide drug screening method, which involves
XX CC combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1),
XX CC exposure to a test compound, and monitoring for disruption of the
XX CC interaction, e.g. by co-precipitation, protein interactive trapping
XX CC or ELISA. Interaction of Bak-2 and viral proteins allows viral
XX CC replication or latency in the absence of apoptosis. Compounds which
XX CC inhibit the interaction may be used as virucide, antitumour or
XX CC diagnostic agents.
XX SQ Sequence 211 AA;

Query Match 97.5%; Score 1075; DB 17; Length 211;
Best Local Similarity 97.2%; Pred. No. 6,8e-110;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRROEGCEPALPSASEQVADTEEEVFYSYFVRHQDEQEAEGVAAAPADPEM 60
DB 1 MASGGGPPRROEGCEPALPSASEQVADTEEEVFYSYFVRHQDEQEAEGVAAAPADPEM 60
QY 61 VTLPLOPSSTMGVQVROLAIIIGDINRRYDSEFOTMLQHLQPTAENAYEFTKIATSLFE 120
DB 61 VTLPLOPSSTMGVQVROLAIIIGDINRRYDSEFOTMLQHLQPTAENAYEFTKIATSLFE 120
QY 121 SGINMGRRVVALLEGYRLALHYVOHGLTGFGLGOVTRFVVDMLHHCIAARIAROGGWAA 180
DB 121 SGINMGRRVVALLEGYRLALHYVOHGLTGFGLGOVTRFVVDMLHHCIAARIAROGGWAA 180
QY 181 LNLGNGPILNLVNLGVVLLGQFVVRREFKS 211
DB 181 LNLGNGPILNLVNLGVVLLGQFVVRREFKS 211

RESULT 8
AAV05432
ID AAV05432 standard; peptide; 208 AA.
XX AC AAV05432;
XX XX
XX DT 02-JUL-1999 (first entry)
XX DE Mouse BAK protein sequence.
XX KW Bcl domain; cell death agonist; bcl homology domain; BCL-2 family;
XX KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
XX KW autoantibody producing cell; cancer; lymphoproliferative condition;
XX KW arthritis; autoimmune disease; therapy.
XX OS Mus sp.
XX PN WO9916787-A1.
XX PD 08-APR-1999.
XX PF 22-SEP-1998; 98WO-US19765.
XX PR 07-OCT-1997; 97US-0946039.
XX PR 26-SEP-1997; 97US-0060133.
XX PA (UNIW ) UNIV WASHINGTON.

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XX PI Kormeyer SJ;
XX DR WPI; 1999-255058/21.
XX PT Bcl homology domain 3 polypeptide
XX PS Disclosure; Fig 21b; 104pp; English.
XX CC This sequence represents the murine BAK protein.
XX CC The invention relates to a bcl homology domain 3 (BH3 domain),
XX CC derived from a proapoptotic member of the BCL-2 family. The
XX CC BH3 polypeptide can be used in a method for promoting apoptosis in a
XX CC target cell, especially where the cell is a cancer cell a virus infected
XX CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
XX CC in therapeutic compositions for treating disease including cancer, other
XX CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
XX CC diseases, which may result from the down regulation of cell death
XX CC regulation.
XX SQ Sequence 208 AA;

Query Match 75.2%; Score 829.5; DB 20; Length 208;
Best Local Similarity 76.3%; Pred. No. 7.1e-83;
Matches 161; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

QY 1 MASGGGPPRROEGCEPALPSASEQVADTEEEVFYSYFVRHQDEQEAEGVAAAPADPEM 60
DB 1 MASGGGPPRROEGCEPALPSASEQVADTEEEVFYSYFVRHQDEQEAEGVAAAPADPEM 57
QY 61 VTLPLOPSSTMGVQVROLAIIIGDINRRYDSEFOTMLQHLQPTAENAYEFTKIATSLFE 120
DB 58 DNLPLEPNSILGQVGRQLALIGDDINRRYDTEFQNLLEQLQPTAGNAYEFTKIATSLFK 117
QY 121 SGINMGRRVVALLEGYRLALHYVOHGLTGFGLGOVTRFVVDMLHHCIAARIAROGGWAA 180
DB 118 SGISMGRRVVALLEGYRLALHYVOHGLTGFGLGOVTRFVVDMLHHCIAARIAROGGWAA 177
QY 181 LNLGNGPILNLVNLGVVLLGQFVVRREFKS 211
DB 178 LNLRRDPILITVNLVIRGVVLLGQFVVRREFKS 208

RESULT 9
AAR77879
ID AAR77879 standard; Protein; 152 AA.
XX AC AAR77879;
XX XX
XX DT 21-NOV-1995 (first entry)
XX DE Human Cdn-1(60-211).
XX KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
XX KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
XX KW shock; lymphoma; eczema.
XX OS Homo sapiens.
XX PN WO9515084-A.
XX PD 08-JUN-1995.
XX PF 30-NOV-1994; 94WO-US13930.
XX PR 07-OCT-1994; 94US-0320157.
XX PR 30-NOV-1993; 93US-0160067.
XX PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX PI Barr PJ, Kiefer MC;
XX DR WPI; 1995-215106/28.

```

XX 22-SEP-1998; 98WO-US19765.
PF
XX 07-OCT-1997; 97US-0946039.
PR
XX 26-SEP-1997; 97US-0060133.
XX
PA (UNIV) UNIV WASHINGTON.
XX
PI Kormeyer SJ;
XX
DR WPI; 1999-255058/21.
XX
XX Bcl homology domain 3 polypeptide
PT
PS Bcl homology domain 3 polypeptide
XX
PS Disclosure; Fig 21b; 104pp; English.
XX
CC This sequence represents the human BAK protein.
CC The invention relates to a bcl homology domain 3 (BH3 domain),
CC derived from a proapoptotic member of the BCL-2 family. The
CC BH3 polypeptide can be used in a method for promoting apoptosis in a
CC target cell, especially where the cell is a cancer cell a virus infected
CC cell or an autotantibody producing cell. The BH3 polypeptide can be used
CC in therapeutic compositions for treating disease including cancer, other
CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC diseases, which may result from the down regulation of cell death
CC regulation.
XX
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 1103; DB 20; Length 211;
Best Local Similarity 100.0%; Pred. No. 5.6e-113;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASGGPGPPROCEGEPALPSASEQVADTEEFVRSYVFYRHQOEAGVAAPADPEM 60
DB 1 MASGGPGPPROCEGEPALPSASEQVADTEEFVRSYVFYRHQOEAGVAAPADPEM 60
QY 61 VTLPPLPSSSTMGGVGRQLAIIGDDINRRYDSEFQTMLOHQPTEANAYEFTKIATSLFE 120
DB 61 VTLPPLPSSSTMGGVGRQLAIIGDDINRRYDSEFQTMLOHQPTEANAYEFTKIATSLFE 120
QY 121 SGINMGRRVALLGFGYRLAHVYOHGLTGFLGQVTRFVVDPMHHCIAHWIAORGWVAA 180
DB 121 SGINMGRRVALLGFGYRLAHVYOHGLTGFLGQVTRFVVDPMHHCIAHWIAORGWVAA 180
QY 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211
DB 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211
RESULT 6
AAR7877
ID AAR7877 standard; Protein; 211 AA.
XX
AC AAR7877;
XX
DT 21-NOV-1995 (first entry)
XX
DE Human Cdn-2.
XX
XX Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
KW shock; lymphoma; eczema.
XX
OS Homo sapiens.
XX
PN WO9515084-A.
XX
PD 08-JUN-1995.
XX
PF 30-NOV-1994; 94WO-US13930.
XX
PR 07-OCT-1994; 94US-0320157.

PR 30-NOV-1993; 93US-0160067.
XX
XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI Barr PJ, Kiefer MC;
XX
DR WPI; 1995-215106/28.
XX
DR N-PSDB; AA095493.
XX
PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
PT related vectors, transformed cells, proteins and antibodies, useful
PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
PT etc.
XX
PS Disclosure; Fig. 5D-E; 66pp; English.
XX
CC Cdn-2 cDNA was isolated from a human placental genomic library
CC using a 950 bp fragment of cdn-1 cDNA. Expression of cdn-2
CC in mouse progenitor B-cell FUS.12 cells decreased IL-3-induced
CC apoptosis. The Cdn-2 protein displayed 97% amino acid identity
CC with Cdn-1 (AAR7876).
XX
XX
SQ Sequence 211 AA;
Query Match 97.5%; Score 1075; DB 16; Length 211;
Best Local Similarity 97.2%; Pred. No. 6.8e-110;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MASGGPGPPROCEGEPALPSASEQVADTEEFVRSYVFYRHQOEAGVAAPADPEM 60
DB 1 MASGGPGPPROCEGEPALPSASEQVADTEEFVRSYVFYRHQOEAGVAAPADPEM 60
QY 61 VTLPPLPSSSTMGGVGRQLAIIGDDINRRYDSEFQTMLOHQPTEANAYEFTKIATSLFE 120
DB 61 VTLPPLPSSSTMGGVGRQLAIIGDDINRRYDSEFQTMLOHQPTEANAYEFTKIATSLFE 120
QY 121 SGINMGRRVALLGFGYRLAHVYOHGLTGFLGQVTRFVVDPMHHCIAHWIAORGWVAA 180
DB 121 SGINMGRRVALLGFGYRLAHVYOHGLTGFLGQVTRFVVDPMHHCIAHWIAORGWVAA 180
QY 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211
DB 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211
RESULT 7
AAM03669
ID AAM03669 standard; Protein; 211 AA.
XX
AC AAM03669;
XX
DT 22-FEB-1997 (first entry)
XX
DE Bak-2 protein.
XX
XX Human; Bak-2; apoptosis; latency; virus replication;
KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
KW drug screening; co-precipitation; ELISA; immunoassay; antibody;
KW protein interactive trapping; virucide; antitumour; diagnostic.
XX
OS Homo sapiens.
XX
PN WO9633416-A1.
XX
PD 24-OCT-1996.
XX
PF 19-APR-1996; 96WO-US05639.
XX
PR 20-APR-1995; 95US-0426529.
XX
PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI Barr PJ, Kiefer MC;

NEW

XX

XX

XX

Year: 1987

PT New isolated human Bcl-Y protein - used to develop prods. for

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: March 27, 2003, 10:44:18 ; Search time 73 Seconds
(without alignments)
385.149 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103
Sequence: 1 MASGGGPPRQEGCEPALP.....LVVLGVLLGQFVRRFFKS 211

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

A.Geneseq.101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1103	100.0	211	17	AAW0368 Bak protein. Homo
3	1103	100.0	211	17	AA81451 Bcl-1 apoptosis-re
4	1103	100.0	211	19	AAW79534 Bak polyprotein.
5	1103	100.0	211	20	AAW05433 Human Bak protein
6	1075	97.5	211	16	AA77877 Human Cdn-2. Homo
7	1075	97.5	211	17	AAW03669 Bak-2 protein. Ho
8	829.5	75.2	208	20	AAW05432 Mouse Bak protein
9	791	71.7	152	16	AA77879 Human Cdn-1(60-211
10	737	66.8	141	16	AA77880 Human Cdn-1(71-211

11	625	56.7	117	19	AAW79535	Truncated Bak poly
12	609	55.2	116	16	AA77881	Human Cdn-1(96-211
13	609	55.2	116	16	AAW79536	Truncated Bak poly
14	284	25.7	52	22	AAW79537	Mammalian Bak alph
15	284	25.7	52	22	AAW79538	Murine Bak peptide
16	192	17.4	239	22	AAW64038	Human Bcl-2 protei
17	191.5	17.4	232	17	AAW01020	Apoptosis-blocking
18	191.5	17.4	232	20	AAW94347	Human Bcl-2 mutant
19	191	17.3	239	17	AAW02383	Human Bcl-2. Homo
20	191	17.3	239	23	AAW05227	Human Bcl-2. Homo
21	190	17.2	239	9	AAW0987	Sequence of bcl-2-
22	190	17.2	239	14	AAW42312	Bcl-2 oncogene pro
23	190	17.2	239	15	AAW47344	Human oncogene bcl
24	190	17.2	239	16	AAW70331	Human bcl-2 protei
25	190	17.2	239	16	AAW71404	Human bcl-2 alpha
26	190	17.2	239	19	AAW40217	Human bcl-2. Homo
27	190	17.2	239	20	AAW87812	A human bcl-2 alph
28	190	17.2	239	21	AAW69203	Amino acid sequenc
29	190	17.2	239	22	AAE08573	Human Bcl-2 protei
30	190	17.2	239	22	AAW64035	Human Bcl-2 protei
31	190	17.2	239	22	AAW64037	Human bcl-2alpha.
32	190	17.2	239	22	AAW74129	Human bcl-2 protei
33	190	17.2	239	22	AAW48288	Human Bcl-2 protei
34	190	17.2	239	22	AAW50537	Protein sequence.
35	190	17.2	239	23	AAW5986	Human bcl2 proto-o
36	190	17.2	272	19	AAW21120	Human bcl-2 protei
37	189.5	17.2	205	16	AAW70332	Human thymus BCL-2
38	189.5	17.2	205	16	AAW68886	Human bcl-2 beta p
39	189.5	17.2	205	16	AAW71405	Human anti-apoptot
40	189.5	17.2	205	18	AAW31529	bcl-2 polyprotein.
41	189.5	17.2	205	20	AAW6319	A human bcl-2 beta
42	189.5	17.2	205	20	AAW87813	Human bcl-2 protei
43	189.5	17.2	205	22	AAW08574	Human bcl-2 protei
44	189.5	17.2	205	22	AAW74130	Human bcl-2beta.
45	189.5	17.2	205	23	AAW75987	Protein sequence.

ALIGNMENTS

RESULT 1	AA77876	standard; Protein: 211 AA.
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AC	21-NOV-1995	(first entry)
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DT		
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DE	Human Cdn-1.	
XX		
KW	Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;	
KW	autoimmune disease; reperfusion injury; hepatitis; osteoporosis;	
KW	shock; lymphoma; eczema.	
XX		
OS	Homo sapiens.	
XX		
PN	W09515084-A.	
XX		
PD	08-JUN-1995.	
XX		
PF	30-NOV-1994;	94WO-US13930.
XX		
PR	07-OCT-1994;	94US-0320157.
XX		
PR	30-NOV-1993;	93US-0160067.
XX		
PA	(LXRB-) LXR BIOTECHNOLOGY INC.	
XX		
PI	Barr PJ, Kiefer MC;	
XX		
DR	WPI, 1995-215106/28.	
XX		
DR	N-PSDB; AA095492.	
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PT	New nucleic acid sequences encoding Cdn apoptosis modulators	- and

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:51:15 ; Search time 27 Seconds

(without alignments)
229.935 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103
Sequence: 1 MASGGPPPPROEGEPALP.....LVVLGVLLGQFVRRFFKS 211

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1103	100.0	211	1	US-08-471-058-10 Sequence 10, Appl1
3	1103	100.0	211	2	US-08-944-530-2 Sequence 2, Appl1
4	1103	100.0	211	3	US-08-471-057-7 Sequence 7, Appl1
5	1103	100.0	211	3	US-08-471-057-10 Sequence 10, Appl1
6	1103	100.0	211	4	US-09-381-488-2 Sequence 2, Appl1
7	1098	99.5	211	1	US-08-321-071A-16 Sequence 16, Appl1
8	1088.5	98.7	210	3	US-08-471-057-22 Sequence 22, Appl1
9	1075	97.5	211	1	US-08-471-058-9 Sequence 9, Appl1
10	1075	97.5	211	1	US-08-471-058-11 Sequence 11, Appl1
11	1075	97.5	211	2	US-08-944-530-4 Sequence 4, Appl1
12	1075	97.5	211	3	US-08-471-057-9 Sequence 9, Appl1
13	1075	97.5	211	3	US-08-471-057-11 Sequence 11, Appl1
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15	737	66.8	141	4	US-08-471-058-23 Sequence 23, Appl1
16	625	56.7	117	4	US-09-381-488-4 Sequence 4, Appl1
17	609	55.2	116	4	US-08-471-058-24 Sequence 24, Appl1
18	609	55.2	116	4	US-09-381-488-5 Sequence 5, Appl1
19	304	27.6	57	1	US-08-321-071A-15 Sequence 15, Appl1
20	285	25.8	54	1	US-08-321-071A-21 Sequence 21, Appl1
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23	191.5	17.4	232	2	US-08-408-095-18 Sequence 18, Appl1
24	191	17.3	239	1	US-08-405-702A-12 Sequence 12, Appl1
25	190	17.2	239	1	US-08-333-565-51 Sequence 51, Appl1
26	190	17.2	239	1	US-08-248-819A-12 Sequence 12, Appl1
27	190	17.2	239	1	US-08-607-269-20 Sequence 20, Appl1

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29	190	17.2	239	1	US-08-690-095-4 Sequence 4, Appl1
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33	190	17.2	239	2	US-08-337-646A-12 Sequence 12, Appl1
34	190	17.2	239	3	US-08-471-057-12 Sequence 12, Appl1
35	190	17.2	239	3	US-09-113-789-4 Sequence 4, Appl1
36	190	17.2	239	3	US-09-080-285-21 Sequence 21, Appl1
37	190	17.2	239	4	US-08-927-326-12 Sequence 12, Appl1
38	190	17.2	239	4	US-08-880-342-15 Sequence 15, Appl1
39	190	17.2	239	4	US-09-234-186-8 Sequence 8, Appl1
40	190	17.2	239	4	US-09-724-426-20 Sequence 20, Appl1
41	190	17.2	239	4	US-09-724-426-21 Sequence 21, Appl1
42	190	17.2	239	5	PCP-US93-05651-5 Sequence 5, Appl1
43	190	17.2	239	5	PCP-US95-04600-20 Sequence 20, Appl1
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ALIGNMENTS

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RESULT 1
US-08-471-058-7
; Sequence 7, Application US/08471058
; Patent No. 5770443
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; GENERAL INFORMATION:
; APPLICANT: Kleier, Michael C.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-471-058-7
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; Sequence 10, Application US/08471058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barf, Philip J.
; TITLE OF INVENTION: NOVEL APROPOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-058-10

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Dd	121	SGINMGRAVVALLFGGYRLATHVYOHGLTGFIQGYTTRVVDENMLHCARLIAORGGVNA	180
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RESULT 3

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US-08-944-530-2
Sequence 2, Application US/08944530
Patent No. 5998131
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: METHODS OF SCREENING FOR THERAPEUTIC
TITLE OF INVENTION: AGENTS USING NOVEL APOPTOSIS-MODULATING PROTEINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,530
FILING DATE: 07-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/426,529
FILING DATE: 20-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23047-20007, 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-944-530-2

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Query Match	100.0%;	Score 1103;	DB 2;	Length 211;
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Db 1 MASGGGPPPPPOECGGEPALPASAEEOYAQOOTEUEFSESYVYVYRHQOEOEAGSVAAPADPEM 60

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Db 61 VTLPLPSPSTMGQVGGRQALAIIGDDINRRYDSEFOTMLQHLQPLAENAYEFTKATLSLE 120

QY 121 SGINMGRRVALLGFGYRLALHYOHGLTGLGQVTRFVVDPMHHCIARWIAORGWVAA 180
Db 121 SGINMGRRVALLGFGYRLALHYOHGLTGLGQVTRFVVDPMHHCIARWIAORGWVAA 180
QY 181 LNLGNGPILNVLVVLGQFVVRFFKS 211
Db 181 LNLGNGPILNVLVVLGQFVVRFFKS 211

RESULT 4

US-08-471-057-7
; Sequence 7, Application US/08471057
; Patent No. 6015687
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,057
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-057-7

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Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 SGINMGRRVALLGFGYRLALHYOHGLTGLGQVTRFVVDPMHHCIARWIAORGWVAA 180
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Db 181 LNLGNGPILNVLVVLGQFVVRFFKS 211

Db 181 LNLGNGPILNVLVVLGQFVVRFFKS 211

RESULT 5

US-08-471-057-10
; Sequence 10, Application US/08471057
; Patent No. 6015687
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,057
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-057-10

Query Match 100.0%; Score 1103; DB 3; Length 211;
Best Local Similarity 100.0%; Pred. No. 6.2e-117;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 VTLPQPSTMGQVROALAIIGDDINRRYDSEFOTMLQHLPRTAENAYEFTKATSLFE 120
Db 61 VTLPQPSTMGQVROALAIIGDDINRRYDSEFOTMLQHLPRTAENAYEFTKATSLFE 120
QY 121 SGINMGRRVALLGFGYRLALHYOHGLTGLGQVTRFVVDPMHHCIARWIAORGWVAA 180
Db 121 SGINMGRRVALLGFGYRLALHYOHGLTGLGQVTRFVVDPMHHCIARWIAORGWVAA 180
QY 181 LNLGNGPILNVLVVLGQFVVRFFKS 211
Db 181 LNLGNGPILNVLVVLGQFVVRFFKS 211
RESULT 6
US-09-381-488-2
; Sequence 2, Application US/09381488
; Patent No. 6441135

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-057-22

Query Match 98.7%; Score 1088.5; DB 3; Length 210;
Best Local Similarity 99.5%; Pred. No. 2.7e-115;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MASGQGPPEPCGEPALPSASEEVOADTEVFPSYFVYFHQOEAEAGVAAPADPEM 60
DB 1 MASGQGPPEPCGEPALPSASEEVOADTEVFPSYFVYFHQOEAEAGVAAPADPEM 60
QY 61 VTLPLOPSSSTMGOVGRQLAIGDINRRYDSEFQTMQLHLOPTAENAYEYFKIATSLFE 120
DB 61 VTLPLOPSSSTMGOVGRQLAIGDINRRYDSEFQTMQLHLOPTAENAYEYFKIATSLFE 120
QY 121 SGINMGVYVALLGFGRALAHVYQHGILGTGLGOVTRFVVDPMILHICIARWIAORGWAA 180
DB 121 SGINMGVYVALLGFGRALAHVYQHGILGTGLGOVTRFVVDPMILHICIARWIAORGWAA 180
QY 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211
DB 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211

RESULT 9
US-08-471-058-9
Sequence 9, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058

FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-471-058-9

Query Match 97.5%; Score 1075; DB 1; Length 211;
Best Local Similarity 97.2%; Pred. No. 9.1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGQGPPEPCGEPALPSASEEVOADTEVFPSYFVYFHQOEAEAGVAAPADPEM 60
DB 1 MASGQGPPEPCGEPALPSASEEVOADTEVFPSYFVYFHQOEAEAGVAAPADPEM 60
QY 61 VTLPLOPSSSTMGOVGRQLAIGDINRRYDSEFQTMQLHLOPTAENAYEYFKIATSLFE 120
DB 61 VTLPLOPSSSTMGOVGRQLAIGDINRRYDSEFQTMQLHLOPTAENAYEYFKIATSLFE 120
QY 121 SGINMGVYVALLGFGRALAHVYQHGILGTGLGOVTRFVVDPMILHICIARWIAORGWAA 180
DB 121 SGINMGVYVALLGFGRALAHVYQHGILGTGLGOVTRFVVDPMILHICIARWIAORGWAA 180
QY 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211
DB 181 LNLGNPILNLVNLVGLGVLLGQFVVRPFKS 211

RESULT 10
US-08-471-058-11
Sequence 11, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-11

Query Match 97.5%; Score 1075; DB 1; Length 211;
Best Local Similarity 97.2%; Pred. No. 9,1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRQECGEPALPSASEEQVAODTEVEFRSYVYFRHQOEAEAGVAAPADPEM 60
DB 1 MASGGGPPRQECGEPALPSASEEQVAODTEVEFRSYVYFRHQOEAEAGVAAPADPEM 60
QY 61 VTLPLOPSSSTMGOVGRQLATIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
DB 61 VTLPLOPSSSTMGOVGRQLATIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
QY 121 SGIMNGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
DB 121 SGIMNGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
QY 181 LNLGNGPLNLVYLVGVLLGQFVVRREFKS 211
DB 181 LNLGNGPLNLVYLVGVLLGQFVVRREFKS 211

RESULT 11

US-08-944-530-4
Sequence 4, Application US/08944530
Patent No. 5998131
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: METHODS OF SCREENING FOR THERAPEUTIC
TITLE OF INVENTION: AGENTS USING NOVEL APOPTOSIS-MODULATING PROTEINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,530
FILING DATE: 07-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/426,529
FILING DATE: 20-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.

REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-944-530-4

Query Match 97.5%; Score 1075; DB 2; Length 211;
Best Local Similarity 97.2%; Pred. No. 9,1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRQECGEPALPSASEEQVAODTEVEFRSYVYFRHQOEAEAGVAAPADPEM 60
DB 1 MASGGGPPRQECGEPALPSASEEQVAODTEVEFRSYVYFRHQOEAEAGVAAPADPEM 60
QY 61 VTLPLOPSSSTMGOVGRQLATIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
DB 61 VTLPLOPSSSTMGOVGRQLATIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
QY 121 SGIMNGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
DB 121 SGIMNGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
QY 181 LNLGNGPLNLVYLVGVLLGQFVVRREFKS 211
DB 181 LNLGNGPLNLVYLVGVLLGQFVVRREFKS 211

RESULT 12

US-08-471-057-9
Sequence 9, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-057-9

Query Match 97.5%; Score 1075; DB 3; Length 211;
Best Local Similarity 97.2%; Pred. No. 9,1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGQGPPEPPROCEGPALPSASEEQVADTEEVRSYVFYHQQEQAEGVAAPADPEM 60
DB 1 MASGQGPPEPPROCEGPALPSASEEQVADTEEVRSYVFYHQQEQAEGVAAPADPEM 60
QY 61 VTLPLOPSSMTGQVGRQLAIIIGDDINRRYDSEFQTMLOHLPDAENAYEFTKATSLFE 120
DB 61 VTLPLOPSSMTGQVGRQLAIIIGDDINRRYDSEFQTMLOHLPDAENAYEFTKATSLFE 120
QY 121 SGINMGVVALLGFYSYRLAHYQGLTGLGQVTRFVVDMLHNCIARMTAQRGWAA 180
DB 121 SGINMGVVALLGFYSYRLAHYQGLTGLGQVTRFVVDMLHNCIARMTAQRGWAA 180
QY 181 LNLGNGPILNLVYLGVVLLGQFVVRREFKS 211
DB 181 LNLGNGPILNLVYLGVVLLGQFVVRREFKS 211

RESULT 13

US-08-471-057-11
Sequence 11, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-057-11

Query Match 97.5%; Score 1075; DB 3; Length 211;
Best Local Similarity 97.2%; Pred. No. 9,1e-114;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGQGPPEPPROCEGPALPSASEEQVADTEEVRSYVFYHQQEQAEGVAAPADPEM 60
DB 1 MASGQGPPEPPROCEGPALPSASEEQVADTEEVRSYVFYHQQEQAEGVAAPADPEM 60
QY 61 VTLPLOPSSMTGQVGRQLAIIIGDDINRRYDSEFQTMLOHLPDAENAYEFTKATSLFE 120
DB 61 VTLPLOPSSMTGQVGRQLAIIIGDDINRRYDSEFQTMLOHLPDAENAYEFTKATSLFE 120
QY 121 SGINMGVVALLGFYSYRLAHYQGLTGLGQVTRFVVDMLHNCIARMTAQRGWAA 180
DB 121 SGINMGVVALLGFYSYRLAHYQGLTGLGQVTRFVVDMLHNCIARMTAQRGWAA 180
QY 181 LNLGNGPILNLVYLGVVLLGQFVVRREFKS 211
DB 181 LNLGNGPILNLVYLGVVLLGQFVVRREFKS 211

RESULT 14

US-08-471-058-22
Sequence 22, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-22

Query Match 71.7%; Score 791; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 8,2e-82;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gencore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:53:34 ; Search time 34 Seconds
(without alignments)
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Title: US-09-633-200-7

Perfect score: 1103
Sequence: 1 MASGGGPPRQECGEPAALP.....LVYLGVLGGFVRRFRFS 211

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep:*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1103	100.0	211	9	US-10-101-482-10
3	1088.5	98.7	210	9	US-10-101-482-22
4	1075	97.5	211	9	US-10-101-482-9
5	1075	97.5	211	9	US-10-101-482-11
6	236	21.4	45	9	US-09-971-980-39
7	130	17.2	239	1	US-08-726-211-5
8	130	17.2	239	9	US-10-101-482-12
9	189.5	17.2	205	1	US-08-726-211-7
10	189.5	17.2	205	10	US-09-952-278-4
11	180	16.3	233	10	US-10-101-482-14
12	180	16.3	233	10	US-09-734-846-2
13	180	16.3	233	10	US-09-952-278-6
14	176	16.0	193	10	US-09-925-674A-7
15	174	15.8	193	10	US-09-925-674A-9
16	169	15.3	155	9	US-10-158-769-1
17	167.5	15.2	190	10	US-09-952-278-2
18	164	14.9	365	9	US-09-809-391-696
19	161.5	14.6	88	9	US-10-101-482-21

20	161	14.6	235	9	US-10-208-155-2	Sequence 2, Appli
21	158.5	14.4	185	10	US-09-864-761-40954	Sequence 40954, A
22	158	14.3	152	9	US-10-158-769-2	Sequence 2, Appli
23	143.5	13.0	226	9	US-10-101-482-15	Sequence 15, Appli
24	143	13.0	192	9	US-10-101-482-13	Sequence 13, Appli
25	143	13.0	331	10	US-09-033-525-2	Sequence 2, Appli
26	132	12.0	213	10	US-09-682-667-2	Sequence 2, Appli
27	127.5	11.6	213	10	US-09-682-667-6	Sequence 6, Appli
28	126	11.4	176	9	US-10-102-806-657	Sequence 657, App
29	116	10.5	172	9	US-10-101-482-16	Sequence 16, Appli
30	112	10.2	134	10	US-09-912-599-6	Sequence 6, Appli
31	109.5	9.9	135	9	US-10-092-750-242	Sequence 242, App
32	107.5	9.7	63	10	US-09-952-278-3	Sequence 3, Appli
33	98	8.9	24	10	US-09-682-667-16	Sequence 16, Appli
34	97	8.8	170	10	US-09-682-667-4	Sequence 4, Appli
35	95	8.6	170	10	US-09-682-667-8	Sequence 8, Appli
36	91	8.3	28	9	US-10-092-750-152	Sequence 152, App
37	90	8.2	16	10	US-09-953-342-22	Sequence 22, Appli
38	87	7.9	187	9	US-10-101-482-17	Sequence 17, Appli
39	86.5	7.8	454	10	US-09-815-242-4877	Sequence 4877, Ap
40	86.5	7.8	474	10	US-09-815-242-10773	Sequence 10773, A
41	86.5	7.8	665	10	US-09-942-447-2	Sequence 2, Appli
42	86	7.8	212	10	US-09-925-300-1577	Sequence 1577, Ap
43	85	7.7	17	9	US-10-092-750-240	Sequence 240, App
44	85	7.7	18	9	US-10-092-750-2	Sequence 2, Appli
45	85	7.7	18	9	US-10-092-750-41	Sequence 41, Appli

ALIGNMENTS

RESULT 1
US-10-101-482-7
Sequence 7, Application US/10101482
Publication No. US2003000837A1

GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
BAR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOENSTER
STREET: 755 Page Mill Road
City: Palo Alto
State: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/101,482
FILING DATE: 18-Mar-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
TOPOLOGY: linear

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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-101-482-7

Query Match
Best Local Similarity 100.0%; Score 1103; DB 9; Length 211;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MASGGGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAEAGVAAPADPEM 60
QY 61 VTLPLOPSSTMGQVGRQALAIIGDDINRRYDSEFOTMLQHLOPTAENAYEFTKATSLFE 120
DB 61 VTLPLOPSSTMGQVGRQALAIIGDDINRRYDSEFOTMLQHLOPTAENAYEFTKATSLFE 120
QY 121 SGIMNGRVALLGFGYRLALHYOHGLTGLGQVTRFVVDFMLHHCIAFWIAORGGWAA 180
DB 121 SGIMNGRVALLGFGYRLALHYOHGLTGLGQVTRFVVDFMLHHCIAFWIAORGGWAA 180
QY 181 LNLGNGPLNLVVLVGLGVLLGQFVVRREFKS 211
DB 181 LNLGNGPLNLVVLVGLGVLLGQFVVRREFKS 211

RESULT 2
US-10-101-482-10
; Sequence 10, Application US/10101482
; Publication No. US2003000837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-101-482-10

Query Match
Best Local Similarity 100.0%; Score 1103; DB 9; Length 211;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAEAGVAAPADPEM 60
DB 1 MASGGGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAEAGVAAPADPEM 60
QY 61 VTLPLOPSSTMGQVGRQALAIIGDDINRRYDSEFOTMLQHLOPTAENAYEFTKATSLFE 120
DB 61 VTLPLOPSSTMGQVGRQALAIIGDDINRRYDSEFOTMLQHLOPTAENAYEFTKATSLFE 120
QY 121 SGIMNGRVALLGFGYRLALHYOHGLTGLGQVTRFVVDFMLHHCIAFWIAORGGWAA 180
DB 121 SGIMNGRVALLGFGYRLALHYOHGLTGLGQVTRFVVDFMLHHCIAFWIAORGGWAA 180
QY 181 LNLGNGPLNLVVLVGLGVLLGQFVVRREFKS 211
DB 181 LNLGNGPLNLVVLVGLGVLLGQFVVRREFKS 211

RESULT 3
US-10-101-482-22
; Sequence 22, Application US/10101482
; Publication No. US2003000837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-101-482-22

Query Match
Best Local Similarity 98.7%; Score 1088.5; DB 9; Length 210;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MASGGGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAEAGVAAPADPEM 60
DB 1 MASGGGPPPPROECGEPALPSASEQVADTEEVFRSYVFRHQOEAEAGVAAPADPEM 60
```

QY 61 VTLPDPSSTMGVGRQLAIGDDINRRYDSEFQTMLOHLPATAENAYEFTKIATSLFE 120
 Db 61 VTLPDPSSTMGVGRQLAIGDDINRRYDSEFQTMLOHLPATAENAYEFTKIATSLFE 120
 QY 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIAHWIAORGWVAA 180
 Db 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIAHWIAORGWVAA 180
 QY 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211
 Db 180 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 210

RESULT 4

US-10-101-482-9
 ; Sequence 9, Application US/10101482
 ; Publication No. US2003000837A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIEFER, MICHAEL C.
 ; BARR, PHILIP J.
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
 ; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; City: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/101,482
 ; FILING DATE: 18-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/320,157
 ; FILING DATE: 07-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: LEHNHARDT, SUSAN K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 23647-20007, 20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 211 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-10-101-482-9

Query Match 97.5%; Score 1075; DB 9; Length 211;
 Best Local Similarity 97.2%; Pred. No. 1.le-102;
 Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRQEGCEPALPSASEQVAODTEEFYRSYVYRHOQOEAGVAAPADPEM 60
 Db 1 MASGGGPPRQEGCEPALPSASEQVAODTEEFYRSYVYRHOQOEAGVAAPADPEM 60
 QY 61 VTLPDPSSTMGVGRQLAIGDDINRRYDSEFQTMLOHLPATAENAYEFTKIATSLFE 120
 Db 61 VTLPDPSSTMGVGRQLAIGDDINRRYDSEFQTMLOHLPATAENAYEFTKIATSLFE 120
 QY 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIAHWIAORGWVAA 180
 Db 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIAHWIAORGWVAA 180

Db 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIAHWIAORGWVAA 180
 QY 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211
 Db 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211

RESULT 5

US-10-101-482-11
 ; Sequence 11, Application US/10101482
 ; Publication No. US2003000837A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIEFER, MICHAEL C.
 ; BARR, PHILIP J.
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
 ; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; City: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/101,482
 ; FILING DATE: 18-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/320,157
 ; FILING DATE: 07-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: LEHNHARDT, SUSAN K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 23647-20007, 20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 211 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-10-101-482-11

Query Match 97.5%; Score 1075; DB 9; Length 211;
 Best Local Similarity 97.2%; Pred. No. 1.le-102;
 Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRQEGCEPALPSASEQVAODTEEFYRSYVYRHOQOEAGVAAPADPEM 60
 Db 1 MASGGGPPRQEGCEPALPSASEQVAODTEEFYRSYVYRHOQOEAGVAAPADPEM 60
 QY 61 VTLPDPSSTMGVGRQLAIGDDINRRYDSEFQTMLOHLPATAENAYEFTKIATSLFE 120
 Db 61 VTLPDPSSTMGVGRQLAIGDDINRRYDSEFQTMLOHLPATAENAYEFTKIATSLFE 120
 QY 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIAHWIAORGWVAA 180
 Db 121 SGINMGRRVVALGFGYRLALHYOHGLTGLGQVTRFVDFMLHHCIAHWIAORGWVAA 180
 QY 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211
 Db 181 LNLGNPILNLVNLVGLVLLGQFVVRREFKS 211

RESULT 6
US-09-971-980-39
; Sequence 39, Application US/09971980
; Patent No. US2002016439A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flavivirus
; TITLE OF INVENTION: Pestiviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 39
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US2002016439A1el Sequence
US-09-971-980-39

Query Match 21.4%; Score 236; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 LHHCIARWIAORGWVAALNLGNGPILNVLVGLVLLGQFVRR 207
DB 1 LHHCIARWIAORGWVAALNLGNGPILNVLVGLVLLGQFVRR 45

RESULT 7
US-08-726-211-5
; Sequence 5, Application US/08726211
; Publication No. US20030012812A1
; GENERAL INFORMATION:
; APPLICANT: Torino, Mar
; APPLICANT: Tait, Ana M.
; APPLICANT: Lopez-Berestein, Gabriel
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
; TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,211
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTXC:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-726-211-5
Query Match 17.2%; Score 190; DB 1; Length 239;
Best Local Similarity 26.4%; Pred. No. 9.6e-12;
Matches 58; Conservative 31; Mismatches 81; Indels 50; Gaps 8;
QY 30 DDEEVRFSYVFYRHQQ---EQEAGV-----AAPA-----DPEMYT 62
DB 10 DREELVYKRIYHKLSQRREMDADYGAAPGAPAGIRFSQPGHTPHPAASRDVART 69
QY 63 IPLQ-PSSTMGVGRQIAIT-----GGINRYSEFQYMLQHLQPTAENAYEY 110
DB 70 SPLQTPAAPGAAGAPALSPVPVYHLRQAGDPSRRYKQDFEAMSSQLHLTPFARGR 129
QY 111 FKIKATSLFEESINGRVALIGFGYRLALHYOHGLTGFAGVTRPVDFMLHICIAWY 170
DB 130 FAVVEBELFRDGVNMGRIYAFEFEGVWCYSVAREKSPCLVDNALMWTYLNKH-LHTW 188
QY 171 IAORGWVAALNLGNGP-----LNLVLVGLVLLG 201
DB 189 IDNGGWAFAVEL-YGPSWRPLDFSWLSLTLTLALVG 227

RESULT 8
US-10-101-482-12
; Sequence 12, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-Oct-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-101-482-12
Query Match 17.2%; Score 190; DB 9; Length 239;
Best Local Similarity 26.4%; Pred. No. 9.6e-12;
Matches 58; Conservative 32; Mismatches 80; Indels 50; Gaps 8;


```

APPLICANT: Nickoloff, Brian J.
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPh-0528
CURRENT FILING DATE: 2000-12-12
PRIORITY APPLICATION NUMBER: 09/277,020
PRIORITY FILING DATE: 1998-03-26
PRIORITY APPLICATION NUMBER: 09/167,921
PRIORITY FILING DATE: 1998-10-07
PRIORITY APPLICATION NUMBER: 09/323,743
PRIORITY FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapiens
US-09-734-846-2

Query Match      16.3%; Score 180; DB 10; Length 233;
Best Local Similarity 28.3%; Pred. No. 9.8e-11;
Matches 43; Conservative 22; Mismatches 71; Indels 16; Gaps 3.

QY 71 MGVGROLAIIIDDDINRRDSEFGMLQLOPTAENAYEFKRIATSLPESGNNGRVVA 130
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 83 MAAYQALKEADEDEFELRRRAFSDDTSOLITPTGTAIYSEFGVYNELFRDGVNNGRIYA 142
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 131 LIGFGYRLALHYOQGLTGFGVYTRFVVDFMLHHCIAFRIAQRGGWAALNL-GNGP-- 187
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 143 FESFGALCVESVDKEMQVLVSRIAMMATYLYNDH-LPEMIOENGWDPFVELYGNMNA 201
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 188 -----ILNVLVLYGVLLGQFVVR 207
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 202 ESRKQGERNRWFLGTGTAVAGVLLGSLFSRK 233
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
US-09-952-278-6
Sequence 6, Application US/09952278
Patent No. US20020137182A1
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. US20020137182A1th Clark Street, Suite 800
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/952,278
FILING DATE: 12-Sep-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. US20020137182A1thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489

```

```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 233 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-952-278-6

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```

Query Match      16.3%; Score 180; DB 10; Length 233;
Best Local Similarity 28.3%; Pred. No. 9.8e-11;
Matches 43; Conservative 22; Mismatches 71; Indels 16; Gaps 3;

```

```

QY 71 MGQVQQLAIIIDDIRRYDSEFQTMLOHPTAENAYEFYFKTATSLFESGIMNGRYVA 130
DB 83 MAAYKQALREAGDEFEELRYRAFSDLTSQHLITPGTAQSEQYVNNELFRDGVNMGRIYA 142
QY 131 LIGFGYRLAHYHGHGLGFGQVTRFYVDMLHHCIAKRWIAQRGVAAALNTL-GNGP-- 187
DB 143 FFSFGALCVESVDKEMQVLVSRILAAWMTYLDNH-LEPWIOENGWDTFVELYGNNA 201
QY 188 -----INLVVLGVLLGQFVRR 207
DB 202 ESRKQGERFNRWFLTGMFTAGVYLLGLFSRK 233

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```

RESULT 14
US-09-925-674A-7
; Sequence 7, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-925-674A-7

```

```

Query Match      16.0%; Score 176; DB 10; Length 193;
Best Local Similarity 28.2%; Pred. No. 1.9e-10;
Matches 57; Conservative 25; Mismatches 86; Indels 34; Gaps 6;

```

```

QY 28 AQTEVFPSYVYRHQOE-----QEAEGVAAPADPEMVTLPLOPSTMGQVROLAIIIGD 83
DB 7  APTRLVADPFGYKLRQGYVCGAGPGEGPADP-----LHQAMRAAGD 51
QY 84 DINRRYDSEFQTMLOHPTAENAYEFYFKTATSLFESGIMNGRYVALLGFGYRLAHYQH 143
DB 52 EFTETRRRTFSDLAQLHVTGPSAQOQRTQVSDLEFGGPMNGRLVAFVFGAALCAESV 111
QY 144 OHGLGFGQVTRFYVDMLHHCIAKRWIAQRGVW-----AALNMGNPILNV 191
DB 112 NKEMEPVGVQVEMWVAY-LETRLADWIIHSSGMAEFYALYGDGALLEARRLREGNNASV 170
QY 192 LVVL-GVLLGQFV-VRRFEKS 211
DB 171 FTVLTGAVALGALVTVGAFAS 192

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RESULT 15
US-09-925-674A-9
; Sequence 9, Application US/09925674A

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; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mouse
US-09-925-674A-9

```

```

Query Match      15.8%; Score 174; DB 10; Length 193;
Best Local Similarity 28.5%; Pred. No. 3.1e-10;
Matches 57; Conservative 24; Mismatches 85; Indels 34; Gaps 6;

```

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QY 30 DTEEVFRSYVYRHQOE-----QEAEGVAAPADPEMVTLPLOPSTMGQVROLAIIIGDI 85
DB 9  DTRALVADPFGYKLRQGYVCGAGPGEGPADP-----LHQAMRAAGDEF 53
QY 86 NRRYDSEFQTMLOHPTAENAYEFYFKTATSLFESGIMNGRYVALLGFGYRLAHYQH 145
DB 54 ETRRRRTFSDLAQLHVTGPSAQOQRTQVSDLEFGGPMNGRLVAFVFGAALCAESVNR 113
QY 146 GLTFGLGQVTRFYVDMLHHCIAKRWIAQRGVW-----AALNMGNPILNV 193
DB 114 EMEPLVGVQVDMWVAY-LETRLADWIIHSSGMAEFYALYGDGALLEARRLREGNNASV 172
QY 194 VL-GVLLGQFV-VRRFEKS 211
DB 173 VLTGAVALGALVTVGAFAS 192

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Search completed: March 27, 2003, 10:58:55
Job time : 34 secs

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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:50:54 / Search time 21 seconds
(without alignments)
965.922 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103
Sequence: 1 MASGGGPGPPROCEGPALP.....LVVLGVLLGPFVRRFRKS 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	211	2	S58873
2	1075	97.5	211	2	S58875
3	189.5	17.2	205	1	TVH0B1
4	189	17.1	239	1	TVH0B1
5	183.5	16.6	233	2	A37332
6	181	16.4	233	2	I49056
7	181	16.4	233	2	S51761
8	180	16.3	233	2	B47557
9	178.5	16.2	199	1	TVMSB1
10	177	16.0	236	1	TVMSA1
11	176.5	16.0	236	1	I53744
12	174.5	15.8	216	2	B37332
13	173.5	15.7	233	2	I67431
14	172.5	15.6	236	2	JC7383
15	170.5	15.5	236	2	I67432
16	167.5	15.2	190	2	A47537
17	164	14.9	227	2	JEO203
18	160.5	14.6	232	2	S24390
19	158.5	14.4	214	2	I49057
20	146	13.2	218	2	B47558
21	143.5	13.0	350	2	A47476
22	143	13.0	192	2	A47538
23	143	13.0	192	2	D47538
24	142	12.9	179	2	JC7255
25	126	11.4	133	2	I53295
26	122	11.1	154	2	I58194
27	116	10.5	172	2	I49449
28	112	10.2	175	2	I39055
29	109	9.9	143	2	I38921

30	107.5	9.7	177	2	S54778	NR-13 protein - qu
31	90.5	8.2	373	2	B75542	conserved hypotet
32	88	8.0	255	2	JC7567	Mcl-1a protein - z
33	86.5	7.8	876	2	AB1177	cation transportin
34	86.5	7.8	876	2	AR1534	band 3-related prote
35	86	7.8	345	2	T08563	band 3-related prote
36	85.5	7.8	1237	2	A56764	hypothetical prote
37	81.5	7.4	416	2	E97579	hypothetical prote
38	81.5	7.4	742	2	T00371	conserved hypotet
39	81	7.3	1021	2	AC2202	hypothetical prote
40	80.5	7.3	272	2	C75560	hypothetical prote
41	80.5	7.3	420	2	D83952	hypothetical prote
42	80.5	7.3	2406	2	A54148	band 3-related prote
43	80.5	7.3	2515	2	S47008	band 3-related prote
44	80	7.3	133	1	GPBP4	band 3 protein - sa
45	80	7.3	865	2	A25104	band 3 protein, no

ALIGNMENTS

RESULT 1
S58873
Bak protein - human
N:Alternate names: bcl-2 homolog; cdn-1 protein
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1996 #sequence-revision 01-Mar-1996 #text-change 08-Oct-1999
C:Accession: S58873; S58872; S58874
R:Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.
Nature 374, 733-736, 1995
A:Title: Induction of apoptosis by the Bcl-2 homologue Bak.
A:Reference number: S58873; MUID:95231653; PMID:7715730
A:Accession: S58873
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-211 <CH1>
A:Cross-references: EMBL:U23765; NID:q758797; PIDN:AAA93066.1; PID:q758798
R:Farooq, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grindham, C.J.; Mar
Nature 374, 731-733, 1995
A:Title: Cloning of a bcl-2 homologue by interaction with adenovirus E1B 19K.
A:Reference number: S58872; MUID:95231652; PMID:7715729
A:Accession: S58872
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <FAR>
A:Cross-references: EMBL:X84213; NID:q804984; PIDN:CAA58997.1; PID:q804985
R:Kiefer, M.C.; Brauer, M.O.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomel, L.D.; Bar
Nature 374, 736-739, 1995
A:Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
A:Reference number: S58874; MUID:95231654; PMID:7715731
A:Accession: S58874
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <KIE>
A:Cross-references: EMBL:U16811; NID:q595923; PIDN:AAA74466.1; PID:q595924
C:Gene: GDB:BAK
A:Gene: GDB:BAK
A:Cross-references: GDB:635887
Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.2e-93;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASGGGPGPPROCEGPALPSAEEOVAODTEVFRRSYFYRHOCEAEAGVAAPADPEM 60
Db 1 MASGGGPGPPROCEGPALPSAEEOVAODTEVFRRSYFYRHOCEAEAGVAAPADPEM 60
QY 61 VTPPLDPSSTMGVQGLAIGDDINRRYDSEFQTMQHLQPTAENAYEFYFKIATSLFE 120
Db 61 VTPPLDPSSTMGVQGLAIGDDINRRYDSEFQTMQHLQPTAENAYEFYFKIATSLFE 120
QY 121 SGINMGVALLGEGYRLALHYQHGLTGFLGVYDFYVDENLHICIAWNIQKRGWAA 180
Db 121 SGINMGVALLGEGYRLALHYQHGLTGFLGVYDFYVDENLHICIAWNIQKRGWAA 180

R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.
 Oncogene Res. 2, 263-275, 1988
 A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
 A:Reference number: A27622; MUID:86217344; PMID:3285301
 A:Accession: A27622
 A:Molecule type: mRNA
 A:Residues: 1-58, 'T', 60-239 <HUA>
 A:Accession: B27622
 A:Molecule type: DNA
 A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA>
 A:Note: the sequence was determined from the germline gene
 C:Comment: Constitutive expression of Bcl2 following t(14;18) chromosomal translocation
 C:Genetics:
 A:Gene: GDB:BCL2
 A:Cross-references: GDB:119031; OMIM:151430
 A:Map position: 18q21.3-18q21.3
 C:Function:
 A:Description: blocks apoptosis in hematopoietic cells
 C:Superfamily: bcl transforming protein
 C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 17.1%; Score 189; DB 1; Length 239;
 Best Local Similarity 26.4%; Pred. No. 8.9e-10;
 Matches 58; Conservative 31; Mismatches 81; Indels 50; Gaps 8;

QY 30 DTEEVRSYVYFHQO---EQEAEV-----AAPA-----DPEMYT 62
 Db 10 DNREIYWKXTHYKLSRGYEMDAGVGAAPGAPGIFSSQPGHTPHPAASRDVART 69
 QY 63 LPLQ-PSSTMGVGRQLAIT-----GDDINRRDSEFQIMLQHOTAENAYEY 110
 Db 70 SPLQPAAGAAGAPALSVPPVHLLTLQAGSDPSKRYRDPFAESSQLHTPTPTARGR 129
 QY 111 FFKIATSLFESGIMNGRVALLGFYRLAHVYQHGLTGFLQVTRFYVDFMLHICIAEW 170
 Db 130 FATVEELRDPVNMGRIVAFEEGVMCESVNREMSPLVDNIALMTEYINRH-LHTW 188

QY 171 IAORGWVAALNIGNPI-----LNVLVVLGVLLG 201
 Db 189 IQDNGMDAFVEL-YGFSMRPLFDPSWLSLKTLLSLALVG 227

RESULT 5
 A37332
 transforming protein (bcl-2-alpha) - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
 C:Accession: A37332; S53453
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
 A:Reference number: A37332; MUID:92375724; PMID:1508712
 A:Accession: A37332
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-233 <EGU>
 A:Cross-references: EMBL:DL1381
 C:Genetics:
 A:Introns: 189/3
 C:Superfamily: bcl transforming protein
 C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 16.6%; Score 183.5; DB 2; Length 233;
 Best Local Similarity 26.9%; Pred. No. 2.7e-09;
 Matches 57; Conservative 35; Mismatches 87; Indels 33; Gaps 10;

QY 2 ASGGC-PGPRROCGEPALPASEBOVADTEEVRSYVYFHQOQAEAGVAAAPADPE 59
 Db 31 AAGEDRPVP-----APA-PAAAPAAVA-----AAGASSHRRPEPPGSAASEVPPA 77
 QY 60 MVTLPLOPSSITMGVGRQLAI--IGDDINRRYDSEFQIMLQHOTAENAYEYFTKATS 117
 Db 78 EGLRAPP-----GYHLLRQAGDEFSSRRYORDEFAQMSGQLHTLPTTAHGRFAVVEE 130

QY 118 LFESGIMNGRVALLGFYRLAHVYQHGLTGFLQVTRFYVDFMLHICIAEWIRQSGW 177
 Db 131 LPRDGVNMGRIVAFEEGVMCESVNREMSPLVDNIALMTEYINRH-LHNMIQDNGW 189

QY 178 VAALN-LGNG--PI-----LNVLVVLGVLLG 201
 Db 190 DAFVELYGNMRPLFDPSWLSLKTLLSLALVG 221

RESULT 6
 bcl-x long - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 C:Accession: I49056; S52866
 R:Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
 J. Immunol. 153, 4388-4398, 1994
 A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
 A:Reference number: I49055; MUID:95052604; PMID:7963517
 A:Accession: I49056
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-233 <RES>
 A:Cross-references: EMBL:U10101; NID:9506647; PIDN:AAA82173.1; PID:9506648
 submitted to the EMBL Data Library, November 1994
 A:Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line th.
 A:Reference number: S52866
 A:Accession: S52866
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-233 <RAM>
 A:Cross-references: EMBL:X83574; NID:9695622; PIDN:CAA58557.1; PID:9695623
 C:Superfamily: bcl transforming protein

Query Match 16.4%; Score 181; DB 2; Length 233;
 Best Local Similarity 28.3%; Pred. No. 4.7e-09;
 Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

QY 71 MGQYRQLAITGDDINRRYDSEFQIMLQHOTAENAYEYFTKATSLEFSGIMNGRVVA 130
 Db 83 MAAYQALREAGDEFLRYRPFSDLTSLQHLITPGTAYQSFQVNLFRDGVNMGRIVA 142

QY 131 LIGFYRLAHVYQHGLTGFLQVTRFYVDFMLHICIAEWIRQSGVVAALN-LGNGP-- 187
 Db 143 FFSFGALCYESVDKEQVLYSRASWMAIYLDH-LDPWIOENGWDFFVDLYGNNA 201

QY 188 -----LNVLVVLGVLLGQFVVR 207
 Db 202 ESRKQDERFNRWFLTGWTAGVVLGSLFSRK 233

RESULT 7
 BCL-X protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
 C:Accession: S51761; S51762
 R:Michaelidis, T.M.
 submitted to the EMBL Data Library, November 1994
 A:Reference number: S51761
 A:Accession: S51761
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <MIC>
 A:Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57886.1; PID:9607177
 A:Experimental source: embryonic; Brain
 A:Accession: S51762
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-125, 189-233 <MI2>
 A:Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57887.1; PID:9607178

QY 75 GROLAI-----IGDDINRRYDSEFOTMLQHLPATAE 105
 Db 62 HREMAARTSPRLPVLATAGPALSPVPCVHLTLRRAGDPSRRYRRDPAEKMSQLHLTPF 121
 QY 106 NAYEFTIATSLFESGINMGWVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHH 165
 Db 122 TARGFATVVEELFDGVMWGRIVAFEEFGGVCVESVNRKMSPLVDNIALMTEYLNRH 181
 QY 166 CIARWIAORGWVVALNLGNGPI-LNVL 192
 Db 182 -LHTWIDONGWDAPVEL-YGPSMRPL 206

RESULT 11
 153744
 gene bcl-2 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
 C:Accession: J53744
 R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
 Gene 140, 291-292, 1994
 A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
 A:Reference number: J53744; MUID:94193015; PMID:8144041
 A:Accession: J53744
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-236 <RES>
 A:Cross-references: GB:J14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
 C:Genetics:
 A:Gene: bcl-2
 C:Superfamily: bcl transforming protein

Query Match 16.0%; Score 176.5; DB 2; Length 236;
 Best Local Similarity 24.2%; Pred. No. 1.2e-08;
 Matches 55; Conservative 31; Mismatches 90; Indels 51; Gaps 7;
 QY 22 ASEQVADTEEVFRSYFYRHQ-----EQBAEGVAAP----- 56
 Db 2 AQAAGTGYDNRKIVMKYHYLSQRYEMDTGDSAPLRAAPPGIFSPQESNRTPAV 61
 QY 57 --DEMYTLPLQPSSTMGVGRQLAI-----GDDINRRYDSEFOTMLQHLPAT 103
 Db 62 HRDAARTSPRLP--LVANAGPALSPVPPVYHLTLRRAGDPSRRYRRDPAEKMSQLHLT 119
 QY 104 AENAYEFTKATSLFESGINMGWVALLGFGYRLALHYQHGLTGFLGQVTRFVDFML 163
 Db 120 PFTARGFATVVEELFDGVMWGRIVAFEEFGGVCVESVNRKMSPLVDNIALMTEYL 179
 QY 164 HHCIARWIAORGWVVALNLGNGPI-----LNVLVVLGVVLLG 201
 Db 180 RH-LHTWIDONGWDAPVEL-YGPSMRPLFDEFSWLSIKTLTLALVG 224

RESULT 12
 B37332
 transforming protein (bcl-2-beta) - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Apr-1998
 C:Accession: B37332; S35452
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues.
 A:Reference number: A37332; MUID:92375724; PMID:1508712
 A:Accession: B37332
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-216 <RGU>
 A:Cross-references: EMBL:DJ1381; EMBL:DJ1382
 C:Superfamily: bcl transforming protein

Query Match 15.8%; Score 174.5; DB 2; Length 216;
 Best Local Similarity 27.3%; Pred. No. 1.7e-08;
 Matches 50; Conservative 27; Mismatches 81; Indels 25; Gaps 7;

QY 2 ASGCG--PGPPROECGPALPSASEBYADTEEVFRSYFYRHQOEQBAEGVAPADPE 59
 Db 31 AAGEIDRPVPP-----AP-PAAPAAVA-----AAGASHHREPPSAASAASEVPA 77
 QY 60 MVTPLQPSSTMGVGRQLAI-----IGDDINRRYDSEFOTMLQHLPATENAYEFTIAT 117
 Db 78 EGLRPAFP-----GVHLLARQAGDEFSRRYQDRFQMSGQLHLPFAHGFVAVEE 130
 QY 118 LFESGINMGWVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIARWIAORGW 177
 Db 131 LFRDGVWGRIVAFEEFGGVCVESVNRKMSPLVDNIALMTEYLNRH-LHNIQONGM 189
 QY 178 VAA 180
 Db 190 VRA 192

RESULT 13
 167431
 BCL-X-Long - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C:Accession: I67431
 R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995
 A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq
 onstitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.
 A:Reference number: I53295; MUID:95129487; PMID:7828536
 A:Accession: I67431
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-233 <RES>
 A:Cross-references: EMBL:J34963; NID:g1004376; PIDN:AAA77686.1; PID:g1004377
 C:Superfamily: bcl transforming protein

Query Match 15.7%; Score 173.5; DB 2; Length 233;
 Best Local Similarity 27.6%; Pred. No. 2.3e-08;
 Matches 48; Conservative 25; Mismatches 78; Indels 23; Gaps 5;
 QY 49 AEGVAPADPEMYTLPLQPSSTMGVGRQLAIIGDDINRRYDSEFOTMLQHLPATENAY 108
 Db 68 ATGSHSSSLAREV-LP-----MAAVKQALREAGDEFELRRRFSDLTSQHLTPGVY 120
 QY 109 EYFTKATSLFESGINMGWVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIA 168
 Db 121 QSEQVYNELFRDGVWGRIVASSSFGALCVESVDKEQVLSKIASMATIYLDH-LE 179
 QY 169 RWIAORGWVVALNLGNGP-----ILNVLVVLGVVLLGQFVVR 207
 Db 180 PWIOENGWMDTFVDLYGNNTAPESRKQGRFNRWFLTGWTVAGVYLLGSLFSRK 233

RESULT 14
 JC7383
 B-cell lymphoma 2 protein - Chinese hamster
 C:Species: Cricetus griseus (Chinese hamster)
 C>Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
 C:Accession: JC7383
 R:Tomovic, M.T.; Christmann, M.; Kaina, B.
 Biochem. Biophys. Res. Commun. 275, 899-903, 2000
 A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
 A:Reference number: JC7383
 A:Contents: Ovary
 A:Accession: JC7383
 A:Molecule type: mRNA
 A:Residues: 1-236 <TOM>
 A:Cross-references: GB:AJ271720
 C:Comment: This protein has anti-apoptotic function, and supports cell survival.
 C:Genetics:
 A:Gene: bcl-2
 C:Superfamily: bcl transforming protein
 C:Keywords: B-cell lymphoma; ovary

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:44:38 ; Search time 13 Seconds

(Without alignments)
673.193 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103

Sequence: 1 MASGGGPGPPROEGGEPALE.....LVVLGVLLGTFVVRERFKS 211

ALIGNMENTS

Scoring table: BLOSUM62

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1103	100.0	211	1	BAK_HUMAN
2	1075	97.5	211	1	BAK2_HUMAN
3	829.5	75.2	208	1	BAK_MOUSE
4	189	17.1	239	1	BCI2_HUMAN
5	186	16.9	229	1	BCI2_BOVIN
6	184	16.7	229	1	BCI2_CHICK
7	183.5	16.6	233	1	BCI2_CHICK
8	181	16.4	233	1	BCI2_MOUSE
9	181	16.4	233	1	BCI2_MOUSE
10	180	16.3	233	1	BCI2_MOUSE
11	179.5	16.3	236	1	BCI2_MOUSE
12	178.5	16.2	236	1	BCI2_MOUSE
13	176	16.0	193	1	BCI2_MOUSE
14	176	16.0	233	1	BCI2_MOUSE
15	172.5	15.6	204	1	BCI2_MOUSE
16	172.5	15.6	236	1	BCI2_MOUSE
17	171	15.5	193	1	BCI2_MOUSE
18	159	14.2	228	1	BCI2_MOUSE
19	146	13.2	218	1	BCI2_MOUSE
20	143	13.0	192	1	BCI2_MOUSE
21	143	13.0	192	1	BCI2_MOUSE
22	141.5	12.8	350	1	BCI2_MOUSE
23	141	12.8	192	1	BCI2_MOUSE
24	134	12.1	192	1	BCI2_MOUSE
25	116	10.5	172	1	BCI2_MOUSE
26	112	10.2	172	1	BCI2_MOUSE
27	109	9.9	143	1	BCI2_MOUSE
28	107.5	9.7	177	1	BCI2_MOUSE
29	97	8.8	892	1	BCI2_MOUSE
30	86	7.8	179	1	BCI2_MOUSE
31	85.5	7.8	1237	1	BCI2_MOUSE
32	85	7.7	179	1	BCI2_MOUSE
33	84	7.6	179	1	BCI2_MOUSE

34	81.5	7.4	742	1	SUN2_HUMAN	Q9uh99 homo sapien
35	81.5	7.4	757	1	DRA_RAT	Q924c9 rattus norv
36	81	7.3	1238	1	B3A2_CAVPO	O920s8 cavia porce
37	80.5	7.3	244	1	CAH_ERMCA	O92538 erwina car
38	80.5	7.3	420	1	YO20_BACHD	O9ka70 bacillus ha
39	80	7.3	133	1	GOP_BPP4	P13058 bacterioph
40	80	7.3	911	1	B3AT_HUMAN	P97738 rattus norv
41	79.5	7.2	432	1	NPX2_RAT	P23347 rattus norv
42	79.5	7.2	1234	1	B3A2_RAT	P47970 cavia porce
43	79	7.2	427	1	APEX_CAVPO	O92ay8 listeria in
44	79	7.2	469	1	MENE_LISIN	P79089 aspergillus
45	79	7.2	498	1	IDHP_ASFNG	

RESULT 1	BAK_HUMAN	STANDARD;	PRT;	211 AA.
AC	Q16611; Q92533;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).			
GN	BAK1 OR BAK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RX	MEDLINE=95231652; PubMed=7715729;			
RA	Farrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T.,			
RA	Glinham C.J., Martinou J.C., Brown R.;			
RT	"Cloning of a bcl-2 homologue by interaction with adenovirus E1B			
RT	19K.";			
RL	Nature 374:731-733(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95231653; PubMed=7715730;			
RA	Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J.,			
RA	Evan G.I., Guild B.C.;			
RT	"Induction of apoptosis by the Bcl-2 homologue Bax.";			
RL	Nature 374:733-736(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95231654; PubMed=7715731;			
RA	Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,			
RA	Tomei L.D., Barr P.J.;			
RT	"Modulation of apoptosis by the widely distributed Bcl-2 homologue			
RT	Bax.";			
RL	Nature 374:736-739(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Williams S.;			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RA	Eguchi H., Hayashi S.;			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	MOTAGENESIS, AND FUNCTION OF BH3 DOMAIN.			
RX	MEDLINE=96091131; PubMed=8521816;			
RA	Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,			
RA	Elangovan B., Chinadurai G., Lutz R.J.;			
RT	"A conserved domain in Bax, distinct from BH1 and BH2, mediates cell			
RT	death and protein binding functions.";			
RL	EMBO J. 14:5589-5596(1995).			
RN	[7]			
RP	STRUCTURE BY NMR OF 72-87.			
RX	MEDLINE=97172562; PubMed=9020082;			

RA Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Mann A.J.,
RA Thompson C.B., Pesik S.W.,
RT "Structure of Bcl-XL-Bak peptide complex: recognition between
RT regulators of apoptosis.";
RL Science 275:983-986(1997).
CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
CC PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC X(L).
CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
CC HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: X84213; CAA58997.1; -;
DR EMBL: U23765; AAA93066.1; -;
DR EMBL: U16811; AAA74466.1; -;
DR EMBL: Z93017; CAB5626.1; -;
DR EMBL: D88397; BAA13606.1; -;
DR EMBL: D88396; BAA13606.1; JOINED.
DR PDB: 1BXL; 29-OCT-97.
DR Genew: HGNC:949; BAK1.
DR MIM: 600516; -;
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane; 3D-structure.
KW DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 211 AA; 23409 MW; A2200E72A46D04E CRC64;

Query Match 100.0%; Score 1103; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 6, 2e-92;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 LNLCNGPILNVLVGLGVLLGQFVVRFFKS 211

RESULT 2
BAK2_HUMAN STANDARD; PRT; 211 AA.
AC Q13041;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bcl-2 homologous antagonist/killer 2 (Apoptosis regulator BAK-2).
GN BCL2L7P1 OR BAK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95231654; PubMed=7715731;
RA Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
RA Tomei L.D., Barr P.J.;
RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue
RT Bak-2".
RL Nature 374:736-739(1995).
CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
CC PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC X(L).
CC -1- SUBCELLULAR LOCATION: Membrane-associated (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
CC HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -1- CAUTION: THIS COULD BE THE PRODUCT OF A PSEDOGENE.
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CC -----
DR EMBL: U16812; AAA74467.1; -;
DR HSP: Q16611; 1BXL.
DR Genew: HGNC:996; BCL2L7P1.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane.
KW DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 POTENTIAL.
SQ SEQUENCE 211 AA; 23411 MW; 703875EC4DCCCB3 CRC64;

Query Match 97.5%; Score 1075; DB 1; Length 211;
Best Local Similarity 97.2%; Pred. No. 2e-89;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;


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Db 1 MASGGGPPRQECGEPALPSASEQVADTEVEFRSRYVFTHHQDEBACAAAPADPEM 60
Qy 61 VTLPQPSSTMGQVGRQALITGDDINRRYDSEFOTMLQHLPTAENAYEFTKIATSLFE 120
Db 61 VTLPQPSSTMGQVGRQALITGDDINRRYDSEFOTMLQHLPTAENAYEFTKIATSLFE 120
Qy 121 SGINMGRRVALLGEGYRLALHYOHGLTGLGQVTRFVNDPMHHCIAIRIAQRGWVAA 180
Db 121 SGINMGRRVALLGEGYRLALHYOHGLTGLGQVTRFVNDPMHHCIAIRIAQRGWVAA 180
Qy 181 LNLGNGPILNVLVGLVGLLQGFVVRREFRS 211
Db 181 LNLGNGPILNVLVGLVGLLQGFVVRREFRS 211

RESULT 3
BAK_MOUSE
ID BAK_MOUSE STANDARD; PRT; 208 AA.
AC 008734;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
GN BAK1 OR BAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss; TISSUE=Liver;
RX MEDLINE=97446138; Pubmed=9299236;
RA Ulrich E., Kaufmann-Zeh A., Hueber A.O., Williamson J.,
RA Chittenden T., Ma A., Evan G.I.;
RT Gene structure, cDNA sequence, and expression of murine Bak, a
RT proapoptotic Bcl-2 family member."
RT Genomics 44:195-200(1997).
RL
CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
CC PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN (BY
CC SIMILARITY).
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC X(L) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: Y1331; CA73684.1; -.
DR HSSP: Q16611; 1BXL.
DR MGD: MGI:1097161; Bak1
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.

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DR PROSITE: PS0062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
FT DOMAIN 71 85 BH3.
FT DOMAIN 114 133 BH1.
FT DOMAIN 166 181 BH2.
FT TRANSMEM 185 202 POTENTIAL.
SQ SEQUENCE 208 AA; 23300 MW; DAFCL1BI60C523C9 CRC64;

Query Match 75.28; Score 829.5; DR 1; Length 208;
Best Local Similarity 76.38; Pred. No. 2,1e-67;
Matches 161; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

Qy 1 MASGGGPPRQECGEPALPSASEQVADTEVEFRSRYVFTHHQDEBACAAAPADPEM 60
Db 1 MASGGGPPRQECGEPALPSASEQVADTEVEFRSRYVFTHHQDEBACAAAPADPEM 60
Qy 61 VTLPQPSSTMGQVGRQALITGDDINRRYDSEFOTMLQHLPTAENAYEFTKIATSLFE 120
Db 58 DNLPLEPSITLGGVGRQALITGDDINRRYDSEFOTMLQHLPTAENAYEFTKIATSLFE 117
Qy 121 SGINMGRRVALLGEGYRLALHYOHGLTGLGQVTRFVNDPMHHCIAIRIAQRGWVAA 180
Db 118 SGISMGRRVALLGEGYRLALHYOHGLTGLGQVTRFVNDPMHHCIAIRIAQRGWVAA 177
Qy 181 LNLGNGPILNVLVGLVGLLQGFVVRREFRS 211
Db 178 LNLGRDPIILNVLVGLVGLLQGFVVRREFRS 208

RESULT 4
BCL2_HUMAN
ID BCL2_HUMAN STANDARD; PRT; 239 AA.
AC P10415; P10416; Q16197; Q13842;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
DE BCL2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RX MEDLINE=86259760; Pubmed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of
RT bcl-2, the gene involved in human follicular lymphoma."
RT Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96: 110 AND 237.
RX MEDLINE=92375724; Pubmed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo."
RN [3]
RP Nucleic Acids Res. 20:4187-4192(1992).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=86196071; Pubmed=2834197;
RA Seto M., Jaeger U., Hockett R.D., Granger W., Bennett S.,
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation
RT of the Bcl-2-ig fusion gene in lymphoma."
RN EMBL J. 7:123-131(1988).

```

RN [5] SOURCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.
 RP MEDLINE-92096610; PubMed-1339299;
 RX Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
 RA "Frequent incidence of somatic mutations in translocated BCL2
 RT oncogenes of non-Hodgkin's lymphomas.";
 RL Blood 79:229-237(1992).
 RN [6]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE-91066924; PubMed-2250705;
 RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
 RT programmed cell death.";
 RL Nature 348:334-336(1990).
 RN [7]
 RP MUTAGENESIS.
 RX MEDLINE-94239528; PubMed-8183370;
 RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;
 RT "Bhl and Bhl domains of Bcl-2 are required for inhibition of
 RT apoptosis and heterodimerization with Bax.";
 RL Nature 369:321-323(1994).
 RN [8]
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.
 RX MEDLINE-98057466; PubMed-9395403;
 RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
 RA Ueno K., Hardwick J.M.;
 RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
 RL Science 278:1966-1968(1997).
 RN [9]
 RP REVIEW ON PHOSPHORYLATION.
 RX MEDLINE-21260650; PubMed-11368354;
 RA Kuwolo P.P., Deng X., May W.S.;
 RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
 RL Leukemia 15:515-522(2001).
 RN [10]
 RP PHOSPHORYLATION BY ASK1/JNK1.
 RX MEDLINE-20036804; PubMed-10567572;
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.;
 RT "Bcl-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
 RT protein kinase pathway normally activated at G(2)/M.";
 RL Mol. Cell. Biol. 19:8469-8478(1999).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (Apaf-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-x(L). Heterodimerization with BAX requires intact BHL and BH2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1 and RAFF-1.
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
 CC are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 CC for interaction with RAFF-1.
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and
 CC occurs during the G2/M phase of the cell cycle. In the absence of
 CC growth factors, Bcl2 appears to be phosphorylated by other protein
 CC kinases such as ERKs and stress-activated kinases.
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity.
 CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type
 CC II chronic lymphatic leukemia) by a chromosomal translocation
 CC t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene

CC regions.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BHL) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -1- DATABASE: NAME=AtLAS Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chromocancer/genes/BCL2ID49.html".
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 CC or send an email to licenselsb-sib.ch).
 CC -----
 CC EMBL: M13994; AAAS1813.1; ALT_SEQ.
 CC EMBL: M13995; AAAS1814.1; ALT_SEQ.
 CC EMBL: M14745; AAAS3591.1; -.
 CC EMBL: X06487; CAA29778.1; -.
 CC EMBL: S72602; AAD14111.1; ALT_SEQ.
 CC PIR: A29409; TYHUA1.
 CC PIR: B29409; TYHUA1.
 CC PIR: A24428; TYHUBC.
 CC PIR: C37332; C37332.
 CC PIR: D37332; D37332.
 CC HSSP: 007817; IMAZ.
 CC Genew: HGNC:990; BCL2.
 CC MIM: 151430; -.
 CC InterPro: IPR002475; BCL2_family.
 CC InterPro: IPR000712; BCL2_BH.
 CC InterPro: IPR003093; BCL2_BH4.
 CC InterPro: IPR004725; BCL2_Reg.
 CC Pfam: PF00452; Bcl-2; 1.
 CC Pfam: PF02180; BH4; 1.
 CC SMART: SM00337; BCL; 1.
 CC SMART: SM00265; BH4; 1.
 CC TIGRFAWS: TIGR00865; Bcl-2; 1.
 CC PROSITE: PS50062; BCL2_FAMILY; 1.
 CC PROSITE: PS01080; BH1; 1.
 CC PROSITE: PS01258; BH2; 1.
 CC PROSITE: PS01259; BH3; 1.
 CC PROSITE: PS01260; BH4_1; 1.
 CC PROSITE: PS00063; BH4_2; 1.
 CC PROSITE: PS50063; BH4_2; 1.
 CC Proto-oncogene; Apoptosis; Alternating splicing; Transmembrane;
 CC Mitochondrium; Phosphorylation; Chromosomal translocation;
 CC Polymorphism; Disease mutation.
 CC DOMAIN 10 30
 CC FT 93 107
 CC DOMAIN 136 155
 CC FT 187 202
 CC DOMAIN 212 233
 CC FT 34 35
 CC SITE 70 70
 CC MOD_RES 196 239
 CC FT 196 239
 CC VARIANT 7 7
 CC FT 7 7
 CC VARIANT 59 59
 CC FT 59 59
 CC VARIANT 93 93
 CC FT 93 93
 CC MUTAGEN 34 34
 CC FT 64 64
 CC MUTAGEN 145 145
 CC FT 145 145
 CC MUTAGEN 168 188
 CC FT 168 188
 CC CONFLICT 48 48
 CC FT 59 59
 CC CONFLICT 59 59
 CC FT 59 59

DE Apoptosis regulator Bcl-X.
 CN BCL2L1 OR BCLX OR BCL-X.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 OX
 RN [1]
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RX MEDLINE=93364977; PubMed=8358789;
 RA Bolse L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
 RA Tuka L.A., Mao X., Nunez G., Thompson C.B.;
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
 RT of apoptotic cell death.";
 RT Cell 74:597-608(1993).
 RN [2]
 RN SEQUENCE FROM N.A. (LONG FORM).
 RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
 RX MEDLINE=97264485; PubMed=9110311;
 RA Vilagrasa X., Mezquita C., Mezquita J.;
 RT "Differential expression of bcl-2 and bcl-x during chicken
 RT spermatogenesis.";
 RT Mol. Reprod. Dev. 47:26-29(1997).
 CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
 CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
 CC ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
 CC ENVELOPE (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
 CC DEVELOPMENT.
 CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
 CC FUNCTION. INTRAC BHL AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
 CC APOPTOTIC ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 CC
 DR EMBL; 223110; GAA80657.1; -;
 DR EMBL; 026645; AAB07677.1; -;
 DR PIR; AA7537; AA7537.
 DR HSSP; P53563; IAR3.
 DR InterPro; IPR002475; BCL2_family.
 DR InterPro; IPR000712; BCL2_BH.
 DR InterPro; IPR003093; BCL2_BH4.
 DR InterPro; IPR004725; BCL2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRfams; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 KW Apoptosis; Transmembrane; Alternative splicing.
 FT DOMAIN 4 24
 FT DOMAIN 82 96 BH4.
 FT DOMAIN 125 144 BH3.
 FT DOMAIN 176 191 BH2.

FT TRANSMEM 206 223 POTENTIAL.
 FT VARSPIC 185 229 ERFVDLYGNNAAEIRKQETFNKMLTGATVAGVLLGSL
 FT
 SQ SEQUENCE 229 AA: 25733 MW: A97D3A4D04C0E9DA CRC64;
 Query Match 16.7%; Score 184; DB 1; Length 229;
 Best Local Similarity 23.9%; Pred. No. 1.9e-09;
 Matches 55; Conservative 33; Mismatches 92; Indels 50; Gaps 6;
 OY 27 VADDTVEFRSVYFYRHQ-----EQEAG-----VVAAPAPENV----- 61
 Db 1 MSSSNRELYIDFVSYKLSRGHCWSELEEDERDPTAEAMDSVLYNGSPWHPACHV 60
 OY 62 -----TLDPQPSSTGQVGRQALIGDDINRRYSEFQTMLOHPTAENAYEFT 112
 Db 61 VNCATVHRSSLEHETVRSADVQALRDAGDEFLRYRAFSDLTSQHLTFPGTAYOSFE 120
 OY 113 KIATSLFESGINKGRVYALLGRTALHAYQHGTLGFGQVTRVDFMLHICARMTA 172
 Db 121 QVNVLEFHGQVNMGRIVAFESFGALCVSDKEMKRVIGRTVSWMTYTLTDH-LDPWIQ 179
 OY 173 QREGVY-----AALNNGNP-----ILNVLVGLGVLLGQFVVR 207
 Db 180 ENCGWERFVDLYGNNAAEIRKQETFNKMLTGATVAGVLLGSLSRK 229
 RESULT 7
 BCL2_CHICK
 ID BCL2_CHICK STANDARD; PRT: 233 AA.
 AC 000709;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 OX
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92375724; PubMed=1508712;
 RA Bucht Y., Ewert D.L., Tsujimoto Y.;
 RT "Isolation and characterization of the chicken bcl-2 gene: expression
 RT in a variety of tissues including lymphoid and neuronal organs in
 RT adult and embryo.";
 RT Nucleic Acids Res. 20:4187-4192(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=B-cell lymphoma;
 RX MEDLINE=92379084; PubMed=1511008;
 RA Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
 RT homologue of the Bcl-2 oncoprotein.";
 RL Biochim. Biophys. Acta 1132:109-113(1992).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling in the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
 CC kidney, heart, ovary and brain, with the highest levels in the
 CC thymus. In the embryo, highly levels expressed in all tissues with
 CC high levels in the bursa of Fabricius.

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CC -1- DOMAIN: The Bcl4 domain is required for anti-apoptotic activity and
CC for interaction with Raf-1 (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D11382; BAA01978.1; -.
DR EMBL: D11381; BAA01978.1; JOINED.
DR EMBL: 211961; CA978018.1; -.
DR PIR: A37332; A37332.
DR PIR: S24390; S24390.
DR HSP: Q07817; IMAZ.
DR InterPro: IPR002475; BCL2 family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004723; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS00062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4.1; 1.
DR PROSITE: PS00063; BH4.2; 1.
DR Apoptosis; Transmembrane; Mitochondrion.
FT DOMAIN 10 30 BH4.
FT DOMAIN 87 101 BH3.
FT DOMAIN 130 149 BH1.
FT DOMAIN 181 196 BH2.
FT TRANSMEM 208 228 POTENTIAL.
FT CONFLICT 64 64 E -> S (IN REF. 2).
FT CONFLICT 67 82 GSAASEVPPAEGLRP -> ARLLVRCPLRGCA
FT CONFLICT 121 121 H -> T (IN REF. 2).
FT CONFLICT 139 139 G -> V (IN REF. 2).
SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6E4C3D CRC64;

Query Match 16.6%; Score 183.5; DB 1; Length 233;
Best Local Similarity 26.9%; Pred. No. 2.2e-09;
Matches 57; Conservative 35; Mismatches 87; Indels 33; Gaps 10;

OY 2 ASGGS--GGPRQEGEGALPSASEQVAQDTEYFRKYVYVYRHQOQDEAGVAAPADPE 59
DB 31 AAGGRRPPVP-----AA-PAAPAAVA-----AAGASSHRPPEPGSAASEVPPA 77
OY 60 MVTPLQPSSTMGVYGRQGLAT--IGDDINRRYDSFEQTMQLHPTLAENAYEFTKIATS 117
DB 78 EGLRAPR-----GVALLARQADESKRYQDFQMSQQLHPTTAGRVAAVEE 130
OY 118 LFESGINKGRVALLGEGYRLALNVYQGLGQVTRFYVDFMLHHCIAKRWIAQSGW 177
DB 131 LFRDGVNMGRIYAFPEEGVACVSVNREMSPLVDNITMTETVLNRR-LHNWIQDNGW 189
OY 178 VAALNL-GNG--PI-----LNVIVLVGVLIG 201
DB 190 DAFVELYGNMRLPDESWISLKTLLSLVIG 221

RESULT 8
BCLX_MOUSE

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ID BCLX_MOUSE STANDARD: PRT; 233 AA.
AC 064373; 060657; Q60658; Q61338;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
OS BCL2L1 OR BCL2L OR BCLX.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2A4B;
RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=95331139; PubMed=7607090;
RA Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L., Boise L.H.,
RT Thompson C.B., Nunez G.;
RL "bcl-xL is the major bcl-x mRNA form expressed during murine
RT development and its product localizes to mitochondria."
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM)).
RC TISSUE=Pre-B cell;
RX MEDLINE=95052604; PubMed=7963517;
RA Fang W., Rivard J.-D., Mueller D.L., Behrens T.W.;
RT "Cloning and molecular characterization of mouse bcl-x in B and T
RT lymphocytes."
RL J. Immunol. 153:4388-4398(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=98051053; PubMed=9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
RT apoptosis in T cells."
RL J. Immunol. 158:4750-4757(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97289584; PubMed=9144489;
RA Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
RT Ohta S., Seidm M.F., Nunez G.;
RL "Genomic organization, promoter region analysis, and chromosome
RT localization of the mouse bcl-x gene."
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VMAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
CC isoform promotes apoptosis.
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE AND PERINUCLEAR
CC ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S),
CC BCL-X(BETA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. WITH HIGHEST LEVELS IN THE
CC BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-
CC TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
CC ACTIVATED.
CC -1- DEVELOPMENTAL STAGE: BCL-X(BETA) IS EXPRESSED IN BOTH EMBRYONAL AND
CC POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN
CC POSTNATAL TISSUES.
CC -1- DOMAIN: The BH1 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.

```

CC -1- PMN: Proteolytically cleaved by caspases during apoptosis (By
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC apoptotic activity (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, X83574; CAA58557.1; -;
CC EMBL, L35049; AAA51039.1; -;
CC EMBL, L35048; AAA51040.1; -;
CC EMBL, U10102; AAA82174.1; -;
CC EMBL, U10101; AAA82173.1; -;
CC EMBL, U10100; AAA82172.1; -;
CC EMBL, U51279; AAC53460.1; -;
CC EMBL, U78031; AAB96881.1; -;
CC EMBL, U78030; AAB96881.1; JOINED.
CC HSSP: P53563; IAF3.
CC MGD: MGI:88139; Bcl2l.
CC InterPro: IPR002475; BCL2_family.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR004725; Bcl2_reg.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM0265; BH4; 1.
CC TIGRFAMs: TIGR00865; bcl-2; 1.
CC PROSITE: PS50062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01259; BH3; 1.
CC PROSITE: PS01260; BH4; 1.
CC PROSITE: PS50063; BH4_2; 1.
CC Apoptosis: Mitochondrion; Alternative splicing; Transmembrane.
CC DOMAIN 4 24
CC FT DOMAIN 86 100 BH4.
CC FT DOMAIN 129 148 BH3.
CC FT DOMAIN 180 195 BH1.
CC FT TRANSMEM 210 226 BH2.
CC FT VARSPPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).
CC FT VARSPPLIC 189 233 DTFVLDYGNNAAESRKQERNNRWFLTGMVAGVLLGSL
CC FT VARSPPLIC 194 233 FSRK -> VRTTPTLCPLACVSLICEHP (IN ISOFORM
CC FT VARSPPLIC 194 233 BCL-X(BETA)).
CC FT VARSPPLIC 194 233 LYGNNAAESRRKQERNNRWFLTGMVAGVLLGSLFSRK
CC FT VARSPPLIC 194 233 -> GHDCMCGSAGITLDSVTRH (IN ISOFORM BCL-
CC FT VARSPPLIC 194 233 X(DELTA-TM)).
CC SQ SEQUENCE 233 AA; 26132 MW; 242DAC798B7E072E CRC64;
CC Query Match 16.4%; Score 181; DB 1; Length 233;
CC Best Local Similarity 28.3%; Pred. No. 3.7e-09;
CC Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

RESULT 9
BCLX_RAT STANDARD: PRT: 233 AA
ID BCLX_RAT P53563; Q62678; P70614; Q62836; Q64087; Q64128;
AC P53563; Q62678; P70614; Q62836; Q64087; Q64128;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L OR BCL2L OR BCLX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC TISSUE=Brain;
RA Michaelidis T.M.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Wasseling S.L., David G.L., Choi S., Velluona M., Hardwick J.M.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC TISSUE=Thymus;
RA MEDLINE=96278736; PubMed=8662675;
RX Shitahara N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;
RT "an additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT unspliced RNA, promotes apoptosis in promyeloid cells.";
RL J. Biol. Chem. 271:13258-13265(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX MEDLINE=95129487; PubMed=7828536;
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT "Expression of members of the Bcl-2 gene family in the immature rat
RT ovary: equine chorionotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=98010630; PubMed=9346936;
RA Artlomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
RA Morikawa K.;
RT "Crystal structure of rat Bcl-xL. Implications for the function of
RT the Bcl-2 protein family.";
RL J. Biol. Chem. 272:27886-27892(1997).
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s) and
CC Bcl-x(beta) isoforms promote apoptosis.
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)
CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
CC SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
CC OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
CC DETECTABLE LEVEL OF BCL-X(S).
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1- PMN: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic

CC activity (By similarity).

CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.

CC - SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

CC -----

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CC -----

DR EMBL: X82537; CA57886.1; -

DR EMBL: X82537; CA57887.1; -

DR EMBL: U10579; AAB19257.1; -

DR EMBL: U72350; AAB17353.1; -

DR EMBL: U72349; AAB17352.1; -

DR EMBL: U34963; AAB17686.1; -

DR EMBL: S76513; AAC60701.1; ALT_INT.

DR EMBL: S78284; AAC60702.1; -

DR PDB: 1AF3; 07-JUL-97.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR000712; Bcl2_BH.

DR InterPro: IPR003093; Bcl2_BH4.

DR InterPro: IPR004725; Bcl2_freg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR TIGRfam: TIGR00865; Bcl-2; 1.

DR PROSITE: PS0062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4; 1.

DR PROSITE: PS0063; BH4_2; 1.

DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;

KM 3D-structure.

FT DOMAIN 4 24 BH4.

FT DOMAIN 86 100 BH3.

FT DOMAIN 129 148 BH1.

FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.

FT VARSPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).

FT VARSPLIC 189 233 DTFVLDYGNNAAESRKQGERNRMFLGMVAGVYLLGSL

FT CONFLICT 6 6 R -> Q (IN REF. 1).

FT CONFLICT 12 12 F -> S (IN REF. 2).

FT CONFLICT 64 64 A -> E (IN REF. 2).

FT CONFLICT 81 81 I -> L (IN REF. 4).

FT CONFLICT 119 119 A -> V (IN REF. 4).

FT CONFLICT 143 144 FF -> SS (IN REF. 4).

FT CONFLICT 199 199 A -> T (IN REF. 4).

FT CONFLICT 201 201 A -> P (IN REF. 4).

FT CONFLICT 233 AA; 26158 MW; 2862B6C5864B8CF CRC64;

SO SEQUENCE

Query Match 16.4%; Score 181; DB 1; Length 233;

Best Local Similarity 28.3%; Pred. No. 3.7e-09;

Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

OY 71 MGQVGNLAIIIGDDINRRDSEFMLOHLOPTAENAVEYFKIATSLFESGINGRAYA 130

DB 83 MAANVKALEADDEFELRRRAFSDLTSLHTPTCTAOSFQVYNEELFRGVNMGRIYA 142

OY 131 LIGFGYRLAHYOHGLGFLGQVTRFVVDLHHCICARMTAORCGWAALNL-CNGP-- 187

DB 143 FFSFGALCVESVDKEMQVIVSRISMAATYINDH-LRPWLOENGMDTFVDLYGNNA 201

OY 168 -----ILNVVLVGLVLLIGFVVR 207

DB 202 ESRKGERENRFLTGATVAGVLLGSLSRSK 233

RESULT 10

BCLX_HUMAN

ID BCLX_HUMAN STANDARD; PRT; 233 AA.

AC 007817; 092976;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apoptosis regulator Bcl-x.

GN BCL2L1 OR BCL2L OR BCLX.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).

RA MEDLINE=93364977; PubMed=8358789;

RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T., Turfa L.A., Mao X., Nunez G., Thompson C.B.;

RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.";

RT Cell 74:597-608(1993).

RL [2]

RP SEQUENCE FROM N.A. (ISOFORM BETA).

RA Inohara N., Ohta S.;

RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.

RN [3]

RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.

RA MEDLINE=95372373; PubMed=7644501;

RA Sedlak T.W., Olvtai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B., Korsmeyer S.J.;

RT "Multiple Bcl-2 family members demonstrate selective dimerizations with Bax.";

RT Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).

RN [4]

RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.

RA MEDLINE=96170038; PubMed=8596636;

RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M., Korsmeyer S.J.;

RT "Bax-independent inhibition of apoptosis by Bcl-XL.";

RL Nature 379:554-556(1996).

RN [5]

RP STRUCTURE BY NMR OF 1-209.

RA MEDLINE=97172562; PubMed=9020082;

RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E., Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Mlin A.J., Thompson C.B., Fesik S.W.;

RT "Structure of Bcl-XL-Bax peptide complex: recognition between regulators of apoptosis.";

RL Science 275:983-986(1997).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.

RA MEDLINE=96256675; PubMed=8692274;

RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E., Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L., Ng S.L., Fesik S.W.;

RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed cell death.";

RT Nature 381:335-341(1996).

RN [7]

RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.

RA MEDLINE=98118550; PubMed=9435230;

RA Clem R.J., Cheng E.H.-Y., Kaip C.L., Kirsch D.G., Ueno K., Takahashi A., Kaetan M.B., Griffin D.E., Earnshaw W.C., Veliona M.A., Hardwick J.M.;

RT "Modulation of cell death by Bcl-XL through caspase interaction.";

RT Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).

CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the voltage-dependent anion channel (VDAC) by binding

to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-X(S) isoform promotes apoptosis.

-1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2. Heterodimerization with BAX does not seem to be required for anti-apoptotic activity.

-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANS AND PERINUCLEAR ENVELOPE (BY SIMILARITY).

-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S) AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING LYMPHOCTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.

-1- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death.

-1- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.

-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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EMBL; Z23116; CAAB0662.1; -

DR EMBL; Z23115; CAAB0661.1; -

DR EMBL; U72398; AAB17354.1; -

DR PDB; 1BXU; 29-OCT-97.

DR PDB; 1LXL; 21-APR-97.

DR PDB; 1MAZ; 21-APR-97.

DR Genew; HGNC:992; BCL2L1.

DR MIM; 600039; -

DR InterPro; IPR002475; BCL2_family.

DR InterPro; IPR000712; Bcl2_BH.

DR InterPro; IPR003093; Bcl2_BH.

DR InterPro; IPR004725; Bcl2_reg.

DR Pfam; PF00452; Bcl-2; 1.

DR SMART; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRFAMs; TIGR00865; bcl-2; 1.

DR PROSITE; PS50062; BCL2_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4; 1.

DR PROSITE; PS50063; BH4_2; 1.

DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane; 3D-structure.

KW 3D-structure.

KW 4.

FT DOMAIN 86 24

FT DOMAIN 86 100

FT DOMAIN 129 148

FT DOMAIN 180 195

FT TRANSMEM 210 226

FT SITE 61 61

FT VARSPPLIC 126 188

FT VARSPPLIC 189 233

FT MUTAGEN 61 61

FT MUTAGEN 131 133

FT MUTAGEN 135 137

MUTAGEN 131 133

MUTAGEN 135 137

ACTIVITY.

GRI->ELN: LOSS OF ANTI-APOPTOTIC ACTIVITY.

G->A: NO HETERODIMERIZATION WITH BAX.

G->E: NO HETERODIMERIZATION WITH BAX.

D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.

D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.

WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY BY ABOUT HALF.

D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.

G->A (IN REF. 1; CAAB0661).

SO SEQUENCE 233 AA; 26049 MW; E09D3CDB51AE9BE CRC64;

Query Match

Best Local Similarity 16.3%; Score 180; DB 1; Length 233;

Matches 43; Conservative 22; Mismatches 71; Indels 16; Gaps 3;

QY 71 MGQVGRQALITDDIRNRDSEFQIMLOHTAENAYEFKITSPEGIMNGRYVA 130

DB 83 MAVKQALREADDEFLRYRAFSDTLSQHTPGTAQSEQVNNELFRDGVNMGRIYA 142

QY 131 LIGFGYRALHYQHGLTGFQVTFVDFMILHICIAFMIAORGWVAALNL-GNGP-- 187

DB 143 FRSFGALCVESVDKEMQVLRIRIAMMATYLNH-LPEWIGENGMDTFVELYGNMAA 201

QY 188 -----LNVVYVGVVLGGQFYVR 207

DB 202 ESRKQGERFRNMFLLTGMTVAGVVLGLSLRSRK 233

RESULT 11

BCL2_MOUSE STANDARD; PRT; 236 AA.

ID BCL2_MOUSE

AC P10417; P10418;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apoptosis regulator Bcl-2.

GN BCL2 OR BCL-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).

RC STRAIN=BALB/C; TISSUE=Liver;

RX MEDLINE=87187643; PubMed=3032455;

RA Negini M., Sillini E., Kozak C., Tsujimoto Y., Croce C.M.;

RT "Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.";

RL Cell 49:455-463(1987).

RN [2]

RP REVISIONS TO 221-222.

RX MEDLINE=92375724; PubMed=1508712;

RA Egnuchi Y., Ewert D.L., Tsujimoto Y.;

RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";

RL Nucleic Acids Res. 20:4187-4192(1992).

RN [3]

RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.

RX MEDLINE=97227291; PubMed=9115213;

RA Ito T., Deng X., Carr B., May W.S. Jr.;

RT "Bcl-2 phosphorylation required for anti-apoptosis function.";

RL J. Biol. Chem. 272:11671-11673(1997).

RN [4]

RP DEPHOSPHORYLATION BY PP2A.

RX MEDLINE=99069407; PubMed=9852076;

RA Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;

RT "Reversible phosphorylation of Bcl2 following interleukin 3 or bryostatins 1 is mediated by direct interaction with protein phosphatase 2A.";

RL J. Biol. Chem. 273:34157-34163(1998).

CC	-1	FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (Apaf-1).
CC	-1	SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity).
CC	-1	SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.
CC	-1	ALTERNATIVE PRODUCTS: 2 isoforms: alpha (shown here) and beta; are produced by alternative splicing.
CC	-1	TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC	-1	DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with Raf-1.
CC	-1	PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.
CC	-1	PTM: Proteolytically cleaved by protein phosphatase 2A (PP2A).
CC	-1	cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.
CC	-1	SIMILARITY: CONSTRAINTS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC	-1	SIMILARITY: CONSTRAINTS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC	-1	SIMILARITY: CONSTRAINTS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC	-1	SIMILARITY: CONSTRAINTS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC	-1	SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC	-1	-----
CC	-1	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-1	-----
DR	EMBL: L31532	AAA37282.1; -
DR	EMBL: M16506	AAA37282.1; JOINED.
DR	EMBL: M16506	AAA37281.1; -
DR	PIR: A25960	TVM5A1.
DR	PIR: B25960	TVM5B1.
DR	PIR: E37332	E37332.
DR	HSSP: Q07817	IMA2.
DR	MGI: MGI:88138	Bcl2.
DR	InterPro: IPR002475	BCL2_family.
DR	InterPro: IPR000712	Bcl12_BH.
DR	InterPro: IPR003093	Bcl12_BH4.
DR	InterPro: IPR004725	Bcl12_reg.
DR	Pfam: PF00452	Bcl-2; 1.
DR	Pfam: PF02180	BH4; 1.
DR	SMART: SMO0337	BCL; 1.
DR	SMART: SMO0265	BH4; 1.
DR	TIGRfams: TIGR00865	Bcl-2; 1.
DR	PROSITE: PS50062	BCL2_FAMILY; 1.
DR	PROSITE: PS01080	BH1; 1.
DR	PROSITE: PS01258	BH2; 1.
DR	PROSITE: PS01259	BH3; 1.
DR	PROSITE: PS01260	BH4_1; 1.
DR	PROSITE: PS50063	BH4_2; 1.
DR	PROSITE: PS50063	BH4_2; 1.
KW	Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; Phosphorylation.	
FT	DOMAIN	10 30 BH4.
FT	DOMAIN	90 104 BH3.
FT	DOMAIN	133 152 BH1.
FT	DOMAIN	184 199 BH2.
FT	TRANSMEM	209 230 POTENTIAL.

FT	SITE	34	35	CLEANAGE (BY CASPASES) (BY SIMILARITY).
FT	MOD_RES	70	70	PHOSPHORYLATION (BY PKC).
FT	VARSPLIC	193	236	DAFVALGSPMSPLPDEFMSLKTLLSLALVAGACITLGAYL
FT				GHR -> VGACTIVE (IN ISOFORM BETA).
SQ	SEQUENCE	236 AA;	26425 MW;	AA05EF6B0765BE0A CRC64;
Query Match				
	Best Local Similarity	16.3%;	Score 179.5;	DB 1; Length 236;
	Matches	55; Conservative	31; Mismatches	92; Indels 47; Gaps
QY	22	ASEEVOADTEVFVSYYVYRRHQDE----	QEAEGVAAP--ADPEWATLPELOP--SSIMGVY	74
Db	2	AOAGRTGIDNRKITVKNITHTYKLRSQREYEMDAGDAADAPLGAAPPTQEIFSFEPSNMPAY		61
QY	75	GRGLAI-----	IGDDINRRYDSEFOTMLQHLOPFAE	105
Db	62	HREMAARTSPLEPLVATAGPALSPYPCVHLLTLRRAGDDFSKRYIKRDRFAEMSQHLHPF		121
QY	106	NAYEYFTYIANSLEFESGJINMGSRVALLGFGYRLALHVVYQHGLTGLGQTVRFVYDFMLHH		165
Db	122	TARGFATVVELELFDGQVNMGRITVAFFEEGGVACVESVNRKMSPLVDNIALIMPEYLNKH		181
QY	166	CIARIIAORGGVALLNLNGNPI-----	LANLVVLGVALLG	201
Db	182	-LHTTIIQDNGGDAAVEL-YGFSMRLPDEFMSLKTLLSLALVAG 224		

	RESULT 12		
BCL2_RAT			
ID	BCL2_RAT	STANDARD:	PRT; 236 AA.
AC	P49950; 062837; Q64032;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-JUN-1997 (Rel. 35, Last sequence update)		
DT	15-NOV-2002 (Rel. 41, Last annotation update)		
DE	Apoptosis regulator Bcl-2.		
GN	BCL2 OR BCL-2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NBRL-taxid=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=94193015; PubMed=8144041;		
RA	Sato T., Irie S., Krajewski S., Reed J.C. ;		
RT	"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";		
RL	Gene 140:291-292(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley; TISSUE=Ovary;		
RX	MEDLINE=95129487; PubMed=7828536;		
RA	Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;		
RT	"Expression of members of the bcl-2 gene family in the immature rat		
RT	ovary: equine chorionic gonadotropin-mediated inhibition of granulosa		
RT	cell apoptosis is associated with decreased bax and constitutive		
RL	bcl-2 and bcl-x along messenger ribonucleic acid levels.";		
RN	Endocrinology 136:232-241(1995).		
RN	[3]		
RP	SEQUENCE OF 19-172 FROM N.A.		
RA	MEDLINE=95059917; PubMed=7969891;		
RA	Castren E., Ohgta Y., Bertzagli M.P., Tzimagiorgis G., Thoenen H.,		
RA	Lindholm D.;		
RT	"bcl-2 messenger RNA is localized in neurons of the developing and		
RT	adult rat brain.";		
RL	Neuroscience 61:165-177(1994).		
-1-	FUNCTION: Suppresses apoptosis in a variety of cell systems		
CC	including factor-dependent lymphohematopoietic and neural cells.		
CC	Regulates cell death by controlling the mitochondrial membrane		
CC	permeability. Appears to function in a feedback loop system with		
CC	caspases. Inhibits caspase activity either by preventing the		
CC	release of cytochrome c from the mitochondria and/or by binding to		
CC	the apoptosis-activating factor (APAF-1).		
-1-	SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and		

Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).

-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

-1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium and in the cortical plate.

-1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

-1- PHOSPHORYLATION: Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity). Cleaved proteolytically cleaved by caspases during apoptosis. The Bcl2 domain, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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CC -----

DR EMBL: L14680; AAA53662.1; -

DR EMBL: U34964; AAA73687.1; -

DR HSSP: Q07817; IMAZ.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR000712; BCL2_BH.

DR InterPro: IPR003093; BCL2_BH4.

DR InterPro: IPR004725; Bcl2_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL; 1.

DR SMART: SM00265; BH4; 1.

DR TIGRFAMs: TIGR00865; bcl-2; 1.

DR PROSITE: PS50062; BCL2_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4_1; 1.

DR PROSITE: PS50063; BH4_2; 1.

DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.

KW DOMAIN 10 30 BH4.

FT DOMAIN 90 104 BH3.

FT DOMAIN 133 152 BH1.

FT DOMAIN 184 199 BH2.

FT TRASMEN 209 230 POTENTIAL.

FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).

FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

FT CONFLICT 42 42 A -> R (IN REF. 2).

FT CONFLICT 157 157 E -> G (IN REF. 1).

FT CONFLICT 164 164 S -> Y (IN REF. 2).

FT CONFLICT 212 212 L -> Q (IN REF. 2).

SO SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;

Query Match 16.2%; Score 178.5; DB 1; Length 236;

Best Local Similarity 24.2%; Pred. No. 6.2e-09; Matches 55; Conservative 31; Mismatches 90; Indels 51; Gaps 7;

QY 22 AAEEDVADTEEFVSFYFRRHQ-----EEAGGVAPA----- 56

DB 2 AAGRGYDNRITVKKIYIKLSQGYEMDQDEDSAPLRAPFTGIRFQESNRTPAV 61

QY 57 --DPEAVTLPLQSSMGVGRQALII-----GDDINRRYDSEFQTMLOHLOPT 103

DB 62 HBDTARTSPLRP--LVNAGPALSPPVPVHLTLRRAGDDFSRRYRRDFEMSQHLIT 119

QY 104 AENAYTFPKIATSLFESSINMGRRVALLGFGYRLALHYQGLGFGYTRFVDFML 163

DB 120 PFTARGFATVVEELFRDGVNMGRIYAFEEFGVGVESVNRKMSPLVDNIALMTETLN 179

QY 164 HHCIAWIAQGGWVAALNLGNGPI-----INVLVLGVLLG 201

DB 180 RH-LHWIDNGMGDAFVEL-YGPSRRPLDFDSWISLITLSIALVIG 224

RESULT 13

ID	BCIW_HUMAN	STANDARD:	PRT:	193 AA.
AC	Q92843:			
DT	01-NOV-1997 (rel. 35, Created)			
DT	01-NOV-1997 (rel. 35, Last sequence update)			
DT	15-JUN-2002 (rel. 41, Last annotation update)			
DE	Apoptosis regulator Bcl-w.			
GN	BCL2L2 OR BCLW OR KIAA0271.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96358615; PubMed-8761287;			
RA	Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,			
RA	Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,			
RT	"Bcl-w, a novel member of the bcl-2 family, promotes cell survival.";			
RL	Oncogene 13:665-675(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=97191544; PubMed-9039502;			
RA	Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,			
RA	Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;			
RT	"Prediction of the coding sequences of unidentified human genes. VI.			
RT	The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by			
RT	analysis of cDNA clones from cell line K6-1 and brain.";			
RL	DNA Res. 3:321-328(1996).			
CC	-1- FUNCTION: PROMOTES CELL SURVIVAL.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MELOID CELL LINES AND			
CC	IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,			
CC	AND SALIVARY GLAND.			
CC	-1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC			
CC	FUNCTION.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.			
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: U59747; AAB09055.1; -			
DR	EMBL: D87461; BAA19666.1; -			
DR	HSSP: Q07817; IMAZ.			

DR Genew; HGNC:995; BCL2L2.
 DR MIM; 601931; .
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR Pfam; PF00452; Bcl-2; 1.
 DR SMART; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR PROSITE; PSS0062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS0063; BH4_2; 1.
 DR Apoptosis.
 FT DOMAIN 9 29 BH4.
 FT DOMAIN 85 104 BH1.
 FT DOMAIN 136 151 BH2.
 SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

Query Match 16.0%; Score 176; DB 1; Length 193;
 Best Local Similarity 28.2%; Pred. No. 8.1e-09;
 Matches 57; Conservative 25; Mismatches 86; Indels 34; Gaps 6;

DB 28 AODEEVEFRSYVFRHQE---QEAEVAAAPDPEMTLPLQPSSTMGVGRQALITGD 83
 DB 7 APTFRALVADPFGYKLRQKYVCGAGREGPADP-----LHQAMRAAGD 51
 QY 84 DINRDSSEFQTMLOHLOPTAENAYEFTKIATSLFESGINMGVALLGFGYRLALHY 143
 DB 52 EFERFRFRPSDLAQLHTVPGSAQRFTQVSEDLFGQSPNMGRLVAFVFAALCASV 111
 QY 144 OHGLTGLGVTRFVVDPMHHCIARWIAORGWV-----AALNIGNPIILNV 191
 DB 112 NKEMEPIVGVGVMMVAV-LETRLADWHSSSGMAEFALYGDALFEARRLRGNWASV 170
 QY 192 LVVL-GVLLGQFV-VRRFFKS 211
 DB 171 RVLVTGVALGALVTGAFAS 192

RESULT 14

BCLX_PIG STANDARD; PRT; 233 AA.
 AC 077737;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Apoptosis regulator Bcl-x.
 GN BCL2L1 OR BCL2L OR BCLX.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99171363; PubMed-10072723;
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darner D.;
 RT "Quantification of cardioprotective gene expression in porcine
 RT short-term hibernating myocardium".
 RL J. Mol. Cell. Cardiol. 31:147-158(1999).
 CC -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
 CC caspases (by similarity). Appears to regulate cell death by
 CC blocking the voltage-dependent anion channel (VDAC) by binding
 CC to it and preventing the release of the caspase activator,
 CC cytochrome c, from the mitochondrial membrane.
 CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (by
 CC similarity). Heterodimerization with BAX does not seem to be
 CC required for anti-apoptotic activity (by similarity).
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
 CC ENVELOPE (BY SIMILARITY).
 CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
 CC The BH1 and BH2 domains are required for both heterodimerization

CC with other Bcl2 family members and for repression of cell death.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis (by
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
 CC apoptotic activity (by similarity).
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----

DR EMBL; AJ001203; CAA04597.1; .
 DR HSSP; Q07817; 1MA2.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFSMS; TIGR00865; bcl-2; 1.
 DR PROSITE; PSS0062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4_1; 1.
 DR PROSITE; PS0063; BH4_2; 1.
 DR Apoptosis; Mitochondrion; Transmembrane.
 FT DOMAIN 4 24 BH4.
 FT DOMAIN 86 100 BH3.
 FT DOMAIN 129 148 BH1.
 FT DOMAIN 180 195 BH2.
 FT TRANSMEM 210 226
 SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 16.0%; Score 176; DB 1; Length 233;
 Best Local Similarity 27.6%; Pred. No. 1e-08;
 Matches 42; Conservative 23; Mismatches 71; Indels 16; Gaps 3;

QY 71 MGQVQQLAIIIGDDINRRYSEFQTMLOHLOPTAENAYEFTKIATSLFESGINMGVVA 130
 DB 83 MAAYQALKEADGDEFELRRRAFSDLTSQHLITPGTAVQSEFQVLELFRDGVMMGRIVA 142
 QY 131 LGFGYRLALHYOGLNGFVTRFVVDPMHHCIARWIAORGWVALLN-GNCP-- 187
 DB 143 FFSFGALCVESVDKEMQVLSRIATWMTATLNDH-LEPWIQENGMDTVVELYGNMAA 201
 QY 188 -----ILNVLVLLGVLLGQFVVR 207
 DB 202 ESRKQGERNNRFLTGMTIAGVLLGSLFSRK 233

RESULT 15

ARL1_XENLA STANDARD; PRT; 204 AA.
 AC 091828;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Apoptosis regulator R11 (XR11).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_Taxid=8355;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Head;
RX MEDLINE-9531613; PubMed-7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
   cell-survival genes.";
RL Gene 158:171-179(1995).
CC -1- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; X82461; CNA57844.1; -.
DR HSSP; Q07817; IMA2.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane.
KW DOMAIN
FT DOMAIN 101 120 BH1.
FT DOMAIN 152 167 BH2.
FT TRANSMEM 181 198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 3BF6BE6DDA4CA03 CRC64;

Query Match 15.6%; Score 172.5; DB 1; Length 204;
Best Local Similarity 24.98; Pred. No. 1.8e-08;
Matches 44; Conservative 35; Mismatches 71; Indels 27; Gaps 4;

QY 57 DEPMVTLPIQPS-----STMG---QVGROLAIIIGDDINRRYDSEFOTMLOHPTA 104
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 29 NRPMPMYLMEPSTSRPGGATGIVEEVLQALLEATEFEFLRYORAFSDITSOLHITQ 88
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 105 ENAYEYFTKIAATSLPESGIMNGRVALLGFGYRLAHYQGLGFLGQVTRFYVDPMH 164
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 89 DTAQSGFOQVMGELEFRDGTMGRIYAFPSFGALCVESANKEMTDLLPRIVQMWNY-LE 147
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 165 HCLARWIAORGGVAAALNIGN-----GPIINVLVYLGVVLLGQFYVRR 207
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 148 HTIQPMQENGWEAFVGLYKNAANAQSRSEGRERGRLLTIVMLTGVALVCYMRRR 204
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

```

Search completed: March 27, 2003, 10:52:49
 Job time : 15 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 27, 2003, 10:50:19 ; Search time 30 Seconds
(without alignments)
1449.198 Million cell updates/sec

Title: US-09-633-200-7
Perfect score: 1103
Sequence: 1 MASGGGPPRQEGEPALP.....LVVLGVLLGQFVRRFFRS 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	839	76.1	209	11	Q9UK59
2	733	66.5	163	6	Q9MWS6
3	452	41.0	151	11	Q91WXS
4	390	35.4	80	6	077738
5	181	16.4	211	13	Q9W6F1
6	181	16.4	217	11	Q9NMF3
7	181	16.4	233	6	Q9MYW4
8	181	16.4	233	11	Q35844
9	180	16.3	233	6	Q9MZS7
10	180	16.3	233	6	Q8SQ42
11	177.5	16.1	236	11	Q923R6
12	177	16.0	233	6	Q9N1A2
13	176	16.0	180	6	Q9BD05
14	174	15.8	180	6	Q9BDX7
15	172	15.6	193	11	Q88396
16	170.3	15.5	204	13	Q90Z82

17	164	14.9	331	11	P97287	P97287 mus musculu
18	162	14.7	178	11	Q9CYW5	Q9CYW5 mus musculu
19	161	14.6	219	11	Q9N36	Q9N36 mus musculu
20	161	14.6	235	11	Q35843	Q35843 mus musculu
21	161	14.6	330	11	Q921P3	Q921P3 mus musculu
22	158.5	14.4	188	4	Q9H1R6	Q9H1R6 mus musculu
23	158.5	14.4	188	11	Q9QW2	Q9QW2 mus musculu
24	155.5	14.1	238	13	Q90Z98	Q90Z98 brachydanio
25	144.5	13.1	350	4	Q9UNJ1	Q9UNJ1 homo sapien
26	143.5	13.0	221	13	Q98UJ3	Q98UJ3 xenopus lae
27	142	12.9	179	4	Q9NYG7	Q9NYG7 homo sapien
28	140	12.7	192	13	Q919N4	Q919N4 brachydanio
29	136	12.3	173	4	Q8WZ49	Q8WZ49 homo sapien
30	134.5	12.2	192	6	Q8SQ43	Q8SQ43 felis silve
31	132.5	12.0	173	11	Q9JKL3	Q9JKL3 rattus norv
32	132	12.0	213	11	Q354Z5	Q354Z5 rattus norv
33	130	11.8	149	6	Q9GMC7	Q9GMC7 ovis aries
34	128.5	11.7	212	4	Q9UMX3	Q9UMX3 homo sapien
35	127.5	11.6	213	4	Q9ULJ32	Q9ULJ32 homo sapien
36	124	11.2	89	13	Q8UWJ1	Q8UWJ1 gallus gall
37	121	11.0	213	13	Q9DGJ5	Q9DGJ5 gallus gall
38	121	11.0	213	13	Q9DGJ5	Q9DGJ5 gallus gall
39	119.5	10.8	218	5	Q9N754	Q9N754 suberites d
40	117	10.6	140	11	Q9ESY3	Q9ESY3 mus musculu
41	117	10.6	172	11	Q55177	Q55177 mus musculu
42	117	10.6	172	11	Q55179	Q55179 mus musculu
43	116.5	10.6	108	4	Q9UHR8	Q9UHR8 homo sapien
44	112	10.2	175	11	Q925A9	Q925A9 rattus norv
45	109.5	9.9	92	4	Q9UHR9	Q9UHR9 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9UK59	PRELIMINARY;	PRT;	209 AA.
AC	Q9UK59;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	BAK protein.			
GN	BAK.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY;			
RA	Itoh T., Itoh A., Pleasure D.;			
RL	Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF250504; AAF71760.1; -.			
DR	HSSP; Q16611; 1BXU.			
DR	InterPro; IPR000712; Bcl2_BH.			
DR	InterPro; IPR002475; BCL2_family.			
DR	Pfam; PF00452; Bcl-2; 1.			
DR	SMART; SM00337; BCL; 1.			
DR	PROSITE; PSS0062; BCL2_FAMILY; 1.			
DR	PROSITE; PS01080; BH1; 1.			
DR	PROSITE; PS01258; BH2; 1.			
DR	PROSITE; PS01259; BH3; 1.			
SO	SEQUENCE 209 AA; 2315 MW; 2493B814B1972421 CRC64;			

Query Match 76.1%; Score 839; DB 11; Length 209;

Best Local Similarity 77.3%; Pred. No. 5.9e-73;

Matches 163; Conservative 23; Mismatches 23; Indels 2; Gaps 2;

QY	1	MASGGGPPRQEGEPALP	PSASEBOVADTEVFYSYFRRHOQBOEGVAAPADPEM	60
DB	1	MASGGGPPRQEGEPALP	AL-SASEQGVADTEVFYSYFYHQQDFETGGAAPANPEM	58
QY	61	VTLPLQPSSTMGVGRQLAII	IGDDINRRYDSEFQTLQHLQPTAENAYEFTKIATSLFE	120

[illegible]

RESULT 2			
Q9MZS6			
ID	Q9MZS6	PRELIMINARY;	PRT; 163 AA.
AC	Q9MZS6;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Bak protein (Fragment).		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OX	Bovidae; Caprinae; Ovis.		
ON	NCBI_Taxid=9940;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=OVARY;		
RA	Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;		
RL	"Bak in the sheep ovary";		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBD databases.		
DR	EMBL: AF164518; AAF8533.1; -.		
DR	HSSP: Q16611; IBXL.		
DR	HSSP: IPR000712; BCL2.BH.		
DR	InterPro: IPR002475; BCL2_family.		
DR	Pfam: PF00452; Bcl-2; 1.		
DR	SMART: SM00337; BCL; 1.		
DR	PROSITE: PS50062; BCL2_FAMILY; 1.		
DR	PROSITE: PS01080; BH1; 1.		
DR	PROSITE: PS01258; BH2; 1.		
DR	PROSITE: PS01259; BH3; 1.		
FT	NON_TER	1	
FT	NON_TER	163	
FT	NON_TER	163	
QO	SEQUENCE	163 AA; 18039 MW; FB35E8A8C53AD5B CRC64;	

[illegible]

RESULT 3	
Q91WX5	
Q91WX5	PRELIMINARY;
Q91WX5	PRT; 151 AA.
AC Q91WX5:	
DT 01-DEC-2001 (TREMBLrel. 19, Created)	
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE N-BAK1.	
CN BAK1.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

OC Mammalia:Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=NEURONAL;
RX MEDLINE=21238300; PubMed=11278671;
RA Sun Y.C., Yu L.Y., Saarma M., Timmusk T., Arumae U.;
RT "Neuron-specific Bcl-2 homolog 3 domain-only splice variant of Bak is
anti-apoptotic in neurons, but pro-apoptotic in non-neuronal cells.";
RL J. Biol. Chem. 276:16240-16247(2001).
DR EMBL; AF402617; AL01876.1; -.
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01259; BH3; UNKNOWN_1.
SQ SEQUENCE 151 AA; 16402 MW; 18c13bFF66e4F3B CRC64;
Query Match 41.0%; Score 452; DB 11; Length 151;
Best Local Similarity 75.0%; Pred. No. 8.5e-36;
Matches 87; Conservative 12; Mismatches 15; Indels 2; Gaps 1;

[illegible]

RESULT 4			
ID	077738	PRELIMINARY;	PRT; 80 AA.
AC	077738;		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Bak protein (fragment).		
GN	BAK.		
OS	Sus scrofa (Pig).		
OC	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.		
OX	NCBI_TaxID=9623;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Battling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;		
RT	"Expression of apoptosis-associated genes in hibernating and stunned		
RT	myocardium of pig."		
RL	Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AJ001204; CAA04598.1; -		
DR	HSSP: O16611. 1BLX.		
DR	InterPro: IPR000712; BCL2_BH.		
DR	InterPro: IPR002475; BCL2_family.		
DR	SMART: SM00452; BCL-2; 1.		
DR	SMART: SM00337; BCL1.		
DR	PROSITE: PS50062; BCL2_FAMILY. 1.		
DR	PROSITE: PS01259; BH3. 1.		
FT	NON_TER 1		
FT	NON_TER 80		
FT	NON_TER 80		
SEQUENCE	80 AA; 8818 MW; FDIAF83BD7D59C86 CRC64;		

	Query Match	35.4%	Score 390;	DB 6;	Length 80;	
	Best Local Similarity	92.5%;	Pred. No. 3.4e-30;			
	Matches 74; Conservative	3;	Mismatches	0;	Gaps	0;
QY	50	ECVAPADPEWNTLTPLQSSSTMGVGGRQLATIGDINRRDYDFEQTMLOHLPENAYE	109			
	:	: : : : : : : : : : :				
Db	1	DGAAPTDPENWTTLPLEFSSTMGVGGRQLAIIAGDIDINRRDYDFEQAMLQHPLENNAYE	60			
QY	110	YFTKTIATSLFESGIMNGRV	129			
	:	: : : : : : : : : :				
Db	61	YFTKIASSLFESGIMNGRV	80			

```

RESULT 5
09M6F1 PRELIMINARY; PRT; 211 AA.
AC 09M6F1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Myeloid cell leukemia protein MCL-1 (Fragment).
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-99190706; PubMed-10090728;
RA Lee R.M., Gillet G., Burnside J., Thomas S.J., Neiman P.;
RT "Role of Nr13 in regulation of programmed cell death in the bursa of
RT Fabricius";
RL Genes Dev. 13:718-728(1999).
RP [2]
RP SEQUENCE FROM N.A.
RA Sofer L., Burnside J.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF120210; AAD31644.1; -.
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR NON_TER 1
SQ SEQUENCE 211 AA; 23143 MW; AAB057C63F92BAC7 CRC64;

Query Match
Best Local Similarity 16.4%; Score 181; DB 13; Length 211;
Matches 59; Conservative 44; Mismatches 81; Indels 40; Gaps 10;

QY 7 PGPPROEGCEPALPSASEEOVAODPEEYFRSYVYRHQOEAGVAAPA---DPEMYT 62
DB 4 PCTP-----PELPDLIDELROESLEILRYL-----REAGGEPEGVKKLPGLG 50
QY 63 LPLOP-----SSTMGOVGQOLAIIGDDINRRYDSEFQTMLOHPTAENAYEFTKIATSL 118
DB 51 GGRGRGASAVMEKALETLRRVGGVQMKHELAFOGKRLRLKIKEDDLOANCEVAQV 110
QY 119 FESGI-NMGCRYVALIGFGYRLALHY---YOHGLTGLGOVTRVVDPMHHCIAARIQA 173
DB 111 FNDGVTNMGRRVYTLISFGAFYAKHLKKSINDKCTSLAGITTAIVSSK-----REWLMS 165
QY 174 RGVVAALNLG-----NGPIINLVVL-GVVLG---QFVVR 208
DB 166 QGWEGFVDFFRVEDLESSINVLMAFAGVAGCAGSLAVMIRKV 209

RESULT 6
09N35 PRELIMINARY; PRT; 217 AA.
AC 09N35;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE B-cell leukemia/lymphoma x (Fragment).
GN BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.

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RC STRAIN-129/SVJ;
RA Yang X.-F., Cantor H.;
RT "Novel cDNA structure and genomic organization of apoptosis regulatory
RT gene Bcl-x-gamma.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF133282; AAK15455.1; -.
DR EMBL; AF133281; AAK15455.1; JOINED.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR NON_TER 1
SQ SEQUENCE 217 AA; 24234 MW; 3B5AE809A7DEF18 CRC64;

Query Match
Best Local Similarity 16.4%; Score 181; DB 11; Length 217;
Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

QY 71 MGQVGQOLAIIGDDINRRYDSEFQTMLOHPTAENAYEFTKIATSLFESGINMGHVA 130
DB 67 MAAYKQALREADDEFELRRRAFSDLTSQLHTPQTAVQSEGVVNELEFRDGVWGRIVA 126
QY 131 LGFGYRLALHYOHGLTGLGOVTRVVDPMHHCIAARIQAQGVVAALNL-GNCP-- 187
DB 127 FFSFGALCVESVDKEMOVLVSRISWMATYLNH-LEPMWIOENGWDVTDVLYGNNA 185
QY 188 -----ILNVLVVLGVVLGQFVVR 207
DB 186 ESRKQGERENRWFILGTMVAGVLLGSLFSRK 217

RESULT 7
09MY4 PRELIMINARY; PRT; 233 AA.
AC 09MY4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Bcl-X.
OS Oryctolagus cuniculus (Rabbit).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RA Knott J.C., Robertson L., James E.R.;
RT "Rabbit Bcl-X.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY005131; AAF88137.1; -.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4.1; 1.
DR PROSITE; PS50063; BH4.2; 1.
DR NON_TER 1
SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

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Query Match 16.4%; Score 181; DB 6; Length 233;
 Best Local Similarity 27.8%; Pred. No. 2.2e-09;
 Matches 49; Conservative 23; Mismatches 80; Indels 24; Gaps 4;

QY 55 PADPENVTLQDSSST-----MGQVQQLAIIIGDDINRRDSEFQMLQHPATAEN 106
 DB 59 PADSPAVNGATGSHSSSIDAREVIMPAVKQALREAGDEFEELRRRAFSDLTSLHTTPT 118
 QY 107 AVEFTKATSLFEESGIMGVVALLFGYRALHYQHGLTGFGQVTRFVVDFMLHHC 166
 DB 119 AYGFSEQVVELFRDGVNMGRIYAFESFGALCVESVDKMEYLVSRIAMMATYLNDR- 177
 QY 167 IARMIARQGVVALNL-GNGP-----ILNVLVGLGVLLGQFVYR 207
 DB 178 LEPWIOENGMDTFVELLYGNNAAESRKGOERENMFELTGMTVAGVLLGSLFSRK 233

RESULT 8

ID 035844 PRELIMINARY; PRT; 233 AA.
 AC 035844;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Bcl-XL.
 GN BCL2L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6/CBA; TISSUE=THYMUS;
 RX MEDLINE=98051053; PubMed=9390087;
 RA Yang X.-F., Weber G.F., Cantor H.;
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates
 apoptosis in T cells."
 RL Immunity 7:629-639(1997).
 DR EMBL: U51278; AAC53459.1; -.
 DR HSSP: P53563; IAF3.
 DR MGD: MGI:88139; BCL2L.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR SMART: SM02180; BH4; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRFAMs: TIGR00865; bcl-2; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4; 1.
 DR PROSITE: PS50063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;

Query Match 16.4%; Score 181; DB 11; Length 233;
 Best Local Similarity 28.3%; Pred. No. 2.2e-09;
 Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

QY 71 MGQVQQLAIIIGDDINRRDSEFQMLQHPATAENAYEFTKATSLFEESGIMGVVAL 130
 DB 83 MAAVKQALREAGDEFEELRRRAFSDLTSLHTTPTAYOSFEQVVELFRDGVNMGRIYA 142
 QY 131 LIGFGYRALHYQHGLTGFGQVTRFVVDFMLHHCIAARMIAORGVVALNL-GNGP-- 187
 DB 143 FFSEFGALCVESVDKEMQVLYSRIAMMATYLNDR-LEPWIOENGMDTFVELLYGNNA 201
 QY 188 -----ILNVLVGLGVLLGQFVYR 207

DB 202 ESRKGEENRNFELTGMTVAGVLLGSLFSRK 233

RESULT 9

ID 09MZ57 PRELIMINARY; PRT; 233 AA.
 AC 09MZ57;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Bcl-x long protein.
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
 RT "Bcl-x in the sheep ovary."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF164517; AAF89532.1; -.
 DR HSSP: P53563; IAF3.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; BH4; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRFAMs: TIGR00865; bcl-2; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4; 1.
 DR PROSITE: PS50063; BH4_2; 1.
 SQ SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;

Query Match 16.3%; Score 180; DB 6; Length 233;
 Best Local Similarity 28.3%; Pred. No. 2.7e-09;
 Matches 43; Conservative 22; Mismatches 71; Indels 16; Gaps 3;

QY 71 MGQVQQLAIIIGDDINRRDSEFQMLQHPATAENAYEFTKATSLFEESGIMGVVAL 130
 DB 83 MAAVKQALREAGDEFEELRRRAFSDLTSLHTTPTAYOSFEQVVELFRDGVNMGRIYA 142
 QY 131 LIGFGYRALHYQHGLTGFGQVTRFVVDFMLHHCIAARMIAORGVVALNL-GNGP-- 187
 DB 143 FFSEFGALCVESVDKEMQVLYSRIAMMATYLNDR-LEPWIOENGMDTFVELLYGNNA 201
 QY 188 -----ILNVLVGLGVLLGQFVYR 207
 DB 202 ESRKGEENRNFELTGMTVAGVLLGSLFSRK 233
 RESULT 10
 ID 08SQ42 PRELIMINARY; PRT; 233 AA.
 AC 08SQ42;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Bcl-XL protein.
 GN BCL-XL.
 OS Felis silvestris catus (Cat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.

